GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: October 13, 2005, 02:43:55 ; Search time 110.575 Seconds
(without alignments)
428.900 Million cell updates/sec

Title: US-10-010-729A-9
Perfect score: 586
Sequence: 1 QSVLTQPPSVSAAPGQKVTI.....SLSAVVFGGGTKLTVLGQPK 114

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1854112 seqs, 416015017 residues

Total number of hits satisfying chosen parameters: 1854112

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*
1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
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6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*
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8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
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13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
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19: /cgn2_6/ptodata/2/pubpaa/US11A_PUBCOMB.pep:*
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22: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	582	99.3	114	14	US-10-010-729-9	Sequence 9, Appli
2	539	92.0	234	14	US-10-194-801C-4	Sequence 4, Appli
3	539	92.0	248	16	US-10-779-461-50	Sequence 50, Appl
4	538	91.8	243	14	US-10-322-673-53	Sequence 53, Appl
5	538	91.8	243	18	US-10-981-465-53	Sequence 53, Appl
6	538	91.8	243	18	US-10-981-621-53	Sequence 53, Appl
7	538	91.8	243	18	US-10-981-673-53	Sequence 53, Appl
8	538	91.8	243	18	US-10-981-691-53	Sequence 53, Appl
9	537	91.6	110	17	US-10-727-155-309	Sequence 309, App
10	537	91.6	110	17	US-10-727-155-311	Sequence 311, App
11	534	91.1	258	10	US-09-880-748-1260	Sequence 1260, Ap
12	534	91.1	258	15	US-10-293-418-1260	Sequence 1260, Ap
13	533	91.0	248	10	US-09-880-748-1246	Sequence 1246, Ap
14	533	91.0	248	15	US-10-293-418-1246	Sequence 1246, Ap
15	532	90.8	112	14	US-10-269-805-10	Sequence 10, Appl
16	530	90.4	255	10	US-09-880-748-1156	Sequence 1156, Ap
17	530	90.4	255	15	US-10-293-418-1156	Sequence 1156, Ap
18	528	90.1	110	17	US-10-727-155-86	Sequence 86, Appl
19	528	90.1	110	17	US-10-727-155-164	Sequence 164, App
20	528	90.1	248	10	US-09-880-748-861	Sequence 861, App
21	528	90.1	248	15	US-10-293-418-861	Sequence 861, App
22	528	90.1	248	16	US-10-779-461-21	Sequence 21, Appl
23	528	90.1	251	10	US-09-880-748-1551	Sequence 1551, Ap
24	528	90.1	251	15	US-10-293-418-1551	Sequence 1551, Ap
25	527.5	90.0	111	14	US-10-269-805-6	Sequence 6, Appli
26	526	89.8	253	10	US-09-880-748-1859	Sequence 1859, Ap
27	526	89.8	253	15	US-10-293-418-1859	Sequence 1859, Ap
28	523	89.2	251	17	US-10-935-290-127	Sequence 127, App
29	522	89.1	244	16	US-10-779-461-4	Sequence 4, Appli
30	522	89.1	248	10	US-09-880-748-1465	Sequence 1465, Ap
31	522	89.1	248	15	US-10-293-418-1465	Sequence 1465, Ap
32	522	89.1	248	18	US-10-981-692-25	Sequence 25, Appl
33	522	89.1	251	10	US-09-880-748-1538	Sequence 1538, Ap
34	522	89.1	251	15	US-10-293-418-1538	Sequence 1538, Ap
35	522	89.1	256	10	US-09-880-748-1015	Sequence 1015, Ap
36	522	89.1	256	15	US-10-293-418-1015	Sequence 1015, Ap
37	521	88.9	123	14	US-10-153-437-6	Sequence 6, Appli
38	521	88.9	130	18	US-10-909-851-28	Sequence 28, Appl
39	520	88.7	248	16	US-10-779-461-53	Sequence 53, Appl
40	520	88.7	248	20	US-11-090-847-111	Sequence 111, App
41	519	88.6	254	10	US-09-880-748-1139	Sequence 1139, Ap
42	519	88.6	254	15	US-10-293-418-1139	Sequence 1139, Ap
43	519	88.6	255	10	US-09-880-748-857	Sequence 857, App
44	519	88.6	255	15	US-10-293-418-857	Sequence 857, App
45	518	88.4	110	15	US-10-440-522-7	Sequence 7, Appli

ALIGNMENTS

RESULT 1
US-10-010-729-9
; Sequence 9, Application US/10010729
; Publication No. US20030185827A1
; GENERAL INFORMATION:
; APPLICANT: Rodriguez, Moses
; APPLICANT: Miller, David J.
; APPLICANT: Pease, Larry R.
; TITLE OF INVENTION: Human IgM Antibodies and Diagnostic and
; TITLE OF INVENTION: Therapeutic Uses Thereof Particularly in the Central Nervous
; TITLE OF INVENTION: System
; FILE REFERENCE: 1199-1-005CIP2
; CURRENT APPLICATION NUMBER: US/10/010,729
; CURRENT FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: 09/730,473
; PRIOR FILING DATE: 2000-12-05
; PRIOR APPLICATION NUMBER: 09/580,787
; PRIOR FILING DATE: 2000-05-30
; PRIOR APPLICATION NUMBER: 09/322,862
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 08/779,784
; PRIOR FILING DATE: 1997-01-07
; PRIOR APPLICATION NUMBER: 08/692,084
; PRIOR FILING DATE: 1996-08-08
; PRIOR APPLICATION NUMBER: 08/236,520
; PRIOR FILING DATE: 1994-04-29
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-010-729-9

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  Best Local Similarity   98.2%;  Pred. No. 1.3e-46;
  Matches  112;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

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Db          1 QSVLTQPPSVSAAPGQKVTISCSGSSSNIGNNFVSWYQQLPGTAPRLLIYDITKRPSGIP 60

Qy         61 DRFSGSKSGTSATLGITGLQTGDEADYYCXTWDSSLSAVVFGGGTKLTVLGQPK 114
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RESULT 2
US-10-194-801C-4
; Sequence 4, Application US/10194801C
; Publication No. US20030143643A1
;   GENERAL INFORMATION:
;        APPLICANT: Sherie L. Morrison
;                   Ramon Montano
;        TITLE OF INVENTION: Rh Antibody
;        NUMBER OF SEQUENCES: 11
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Shapiro & Dupont LLP
;             STREET: 233 Wilshire Boulevard, Suite 700
;             CITY: Santa Monica
;             STATE: CA
;             COUNTRY: USA
;             ZIP: 90067
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy Disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: Windows 2000
;             SOFTWARE: MS Word
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/194,801C
;             FILING DATE: 11-Mar-2003
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 09/372,425
;             FILING DATE: August 11, 1999
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Oldenkamp, David J.
;             REGISTRATION NUMBER: 29,421
;             REFERENCE/DOCKET NUMBER: 0180.0033
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (310) 319-5411
;             TELEFAX: (310) 319-5401
;   INFORMATION FOR SEQ ID NO: 4:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 234 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: Light chain - AA
;        SEQUENCE DESCRIPTION: SEQ ID NO: 4
US-10-194-801C-4

  Query Match             92.0%;  Score 539;  DB 14;  Length 234;
  Best Local Similarity   89.5%;  Pred. No. 2.7e-42;
  Matches  102;  Conservative    6;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 QSVLTQPPSVSAAPGQKVTISCSGSSSNIGNNFVSWYQQLPGTAPXLLIYDITKRPSGIP 60
              ||||||||||||||||||||||||||||||:|||||  ||||| |||||  :||||||
Db         19 QSVLTQPPSVSAAPGQKVTISCSGSSSNIGNNYVSWYQHFPGTAPKLLIYDNNQRPSGIP 78

Qy         61 DRFSGSKSGTSATLGITGLQTGDEADYYCXTWDSSLSAVVFGGGTKLTVLGQPK 114
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Db         79 DRFSGSKSGTSATLGITGLQTGDEADYYCGTWNSSLSAVLFGGGTEVTVLGQPK 132


RESULT 3
US-10-779-461-50
; Sequence 50, Application US/10779461
; Publication No. US20040166544A1
; GENERAL INFORMATION:
;  APPLICANT: Morton, Philip A
;  TITLE OF INVENTION: ANTIBODIES TO c-MET FOR THE TREATMENT OF CANCERS
;  FILE REFERENCE: 00980/1
;  CURRENT APPLICATION NUMBER: US/10/779,461
;  CURRENT FILING DATE:  2004-02-13
;  PRIOR APPLICATION NUMBER: 60/447,073
;  PRIOR FILING DATE: 2003-02-13
;  NUMBER OF SEQ ID NOS: 161
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 50
;   LENGTH: 248
;   TYPE: PRT
;   ORGANISM: artificial
;   FEATURE:
;   OTHER INFORMATION: phage display generated human antibody
US-10-779-461-50

  Query Match             92.0%;  Score 539;  DB 16;  Length 248;
  Best Local Similarity   92.8%;  Pred. No. 2.9e-42;
  Matches  103;  Conservative    3;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 QSVLTQPPSVSAAPGQKVTISCSGSSSNIGNNFVSWYQQLPGTAPXLLIYDITKRPSGIP 60
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Db        138 QSVVTQPPSVSAAPGQKVTISCSGSSSNIGNNYVSWYKQLPGTAPKLLIYDNNKRPSGIP 197

Qy         61 DRFSGSKSGTSATLGITGLQTGDEADYYCXTWDSSLSAVVFGGGTKLTVLG 111
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Db        198 DRFSGSKSGTSATLGITGLQTGDEADYYCGTWDSSLSGVVFGGGTKLTVLG 248


RESULT 4
US-10-322-673-53
; Sequence 53, Application US/10322673
; Publication No. US20030180296A1
; GENERAL INFORMATION:
;  APPLICANT: Salcedo et al.
;  TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
;  TITLE OF INVENTION:  Receptors
;  FILE REFERENCE: PF585
;  CURRENT APPLICATION NUMBER: US/10/322,673
;  CURRENT FILING DATE:  2002-12-19
;  PRIOR APPLICATION NUMBER: 60/341,237
;  PRIOR FILING DATE: 2001-12-20
;  PRIOR APPLICATION NUMBER: 60/369,877
;  PRIOR FILING DATE: 2002-04-05
;  PRIOR APPLICATION NUMBER: 60/384,828
;  PRIOR FILING DATE: 2002-06-04
;  PRIOR APPLICATION NUMBER: 60/396,591
;  PRIOR FILING DATE: 2002-07-18
;  PRIOR APPLICATION NUMBER: 60/403,370
;  PRIOR FILING DATE: 2002-08-15
;  PRIOR APPLICATION NUMBER: 60/425,737
;  PRIOR FILING DATE: 2002-11-13
;  NUMBER OF SEQ ID NOS: 72
; SEQ ID NO 53
;   LENGTH: 243
;   TYPE: PRT
;   ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: CM085C11 scFv
US-10-322-673-53

  Query Match             91.8%;  Score 538;  DB 14;  Length 243;
  Best Local Similarity   91.9%;  Pred. No. 3.5e-42;
  Matches  102;  Conservative    5;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 QSVLTQPPSVSAAPGQKVTISCSGSSSNIGNNFVSWYQQLPGTAPXLLIYDITKRPSGIP 60
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Db        133 QSVLTQPPSVSAAPGQKVTISCSGSTSNIGNNYVSWYQQVPGTAPKLLIYDNNKRPSGIP 192
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Qy          61 DRFSGSKSGTSATLGITGLQTGDEADYYCXTWDSSLSAVVFGGGTKLTVLG 111
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Db         193 DRFSGSKSGTSATLGITGLQTGDEADYYCGTWDSSLSALVFGGGTKVTVLG 243


RESULT 5
US-10-981-465-53
; Sequence 53, Application US/10981465
; Publication No. US20050214205A1
; GENERAL INFORMATION:
;  APPLICANT: Salcedo et al.
;  TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
;  TITLE OF INVENTION:  Receptors
;  FILE REFERENCE: PF585P1
;  CURRENT APPLICATION NUMBER: US/10/981,465
;  CURRENT FILING DATE:  2004-11-05
;  PRIOR APPLICATION NUMBER: 60/608,386
;  PRIOR FILING DATE: 2004-09-10
;  PRIOR APPLICATION NUMBER: PCT/US04/013900
;  PRIOR FILING DATE: 2004-05-05
;  PRIOR APPLICATION NUMBER: 60/468,092
;  PRIOR FILING DATE: 2003-05-06
;  PRIOR APPLICATION NUMBER: 60/495,140
;  PRIOR FILING DATE: 2003-08-15
;  PRIOR APPLICATION NUMBER: 10/322,673
;  PRIOR FILING DATE: 2002-12-19
;  PRIOR APPLICATION NUMBER: 60/369,877
;  PRIOR FILING DATE: 2002-04-05
;  PRIOR APPLICATION NUMBER: 60/384,828
;  PRIOR FILING DATE: 2002-06-04
;  PRIOR APPLICATION NUMBER: 60/396,591
;  PRIOR FILING DATE: 2002-07-18
;  PRIOR APPLICATION NUMBER: 60/403,370
;  PRIOR FILING DATE: 2002-08-15
;  PRIOR APPLICATION NUMBER: 60/425,737
;  PRIOR FILING DATE: 2002-11-13
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 76
; SEQ ID NO 53
;   LENGTH: 243
;   TYPE: PRT
;   ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: CM085C11 scFv
US-10-981-465-53

  Query Match             91.8%;  Score 538;  DB 18;  Length 243;
  Best Local Similarity   91.9%;  Pred. No. 3.5e-42;
  Matches  102;  Conservative    5;  Mismatches    4;  Indels    0;  Gaps    0;

Qy           1 QSVLTQPPSVSAAPGQKVTISCSGSSSNIGNNFVSWYQQLPGTAPXLLIYDITKRPSGIP 60
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Db         133 QSVLTQPPSVSAAPGQKVTISCSGSTSNIGNNYVSWYQQVPGTAPKLLIYDNNKRPSGIP 192

Qy          61 DRFSGSKSGTSATLGITGLQTGDEADYYCXTWDSSLSAVVFGGGTKLTVLG 111
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Db         193 DRFSGSKSGTSATLGITGLQTGDEADYYCGTWDSSLSALVFGGGTKVTVLG 243


RESULT 6
US-10-981-621-53
; Sequence 53, Application US/10981621
; Publication No. US20050214206A1
; GENERAL INFORMATION:
;  APPLICANT: Salcedo et al.
;  TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
;  TITLE OF INVENTION:  Receptors
;  FILE REFERENCE: PF585P1D1
;  CURRENT APPLICATION NUMBER: US/10/981,621
;  CURRENT FILING DATE:  2004-11-05
;  PRIOR APPLICATION NUMBER: 60/608,386
;  PRIOR FILING DATE: 2004-09-10
;  PRIOR APPLICATION NUMBER: PCT/US04/013900
;  PRIOR FILING DATE: 2004-05-05
;  PRIOR APPLICATION NUMBER: 60/468,092
;  PRIOR FILING DATE: 2003-05-06
;  PRIOR APPLICATION NUMBER: 60/495,140
;  PRIOR FILING DATE: 2003-08-15
;  PRIOR APPLICATION NUMBER: 10/322,673
;  PRIOR FILING DATE: 2002-12-19
;  PRIOR APPLICATION NUMBER: 60/369,877
;  PRIOR FILING DATE: 2002-04-05
;  PRIOR APPLICATION NUMBER: 60/384,828
;  PRIOR FILING DATE: 2002-06-04
;  PRIOR APPLICATION NUMBER: 60/396,591
;  PRIOR FILING DATE: 2002-07-18
;  PRIOR APPLICATION NUMBER: 60/403,370
;  PRIOR FILING DATE: 2002-08-15
;  PRIOR APPLICATION NUMBER: 60/425,737
;  PRIOR FILING DATE: 2002-11-13
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 76
; SEQ ID NO 53
;   LENGTH: 243
;   TYPE: PRT
;   ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: CM085C11 scFv
US-10-981-621-53

  Query Match             91.8%;  Score 538;  DB 18;  Length 243;
  Best Local Similarity   91.9%;  Pred. No. 3.5e-42;
  Matches  102;  Conservative    5;  Mismatches    4;  Indels    0;  Gaps    0;

Qy           1 QSVLTQPPSVSAAPGQKVTISCSGSSSNIGNNFVSWYQQLPGTAPXLLIYDITKRPSGIP 60
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Db         133 QSVLTQPPSVSAAPGQKVTISCSGSTSNIGNNYVSWYQQVPGTAPKLLIYDNNKRPSGIP 192

Qy          61 DRFSGSKSGTSATLGITGLQTGDEADYYCXTWDSSLSAVVFGGGTKLTVLG 111
               ||||||||||||||||||||||||||||| |||||||:|||||||:||||
Db         193 DRFSGSKSGTSATLGITGLQTGDEADYYCGTWDSSLSALVFGGGTKVTVLG 243


RESULT 7
US-10-981-673-53
; Sequence 53, Application US/10981673
; Publication No. US20050214207A1
; GENERAL INFORMATION:
;  APPLICANT: Salcedo et al.
;  TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
;  TITLE OF INVENTION:  Receptors
;  FILE REFERENCE: PF585P1D2
;  CURRENT APPLICATION NUMBER: US/10/981,673
;  CURRENT FILING DATE:  2004-11-05
;  PRIOR APPLICATION NUMBER: 60/608,386
;  PRIOR FILING DATE: 2004-09-10
;  PRIOR APPLICATION NUMBER: PCT/US04/013900
;  PRIOR FILING DATE: 2004-05-05
;  PRIOR APPLICATION NUMBER: 60/468,092
;  PRIOR FILING DATE: 2003-05-06
;  PRIOR APPLICATION NUMBER: 60/495,140
;  PRIOR FILING DATE: 2003-08-15
;  PRIOR APPLICATION NUMBER: 10/322,673
;  PRIOR FILING DATE: 2002-12-19
;  PRIOR APPLICATION NUMBER: 60/369,877
;  PRIOR FILING DATE: 2002-04-05
;  PRIOR APPLICATION NUMBER: 60/384,828
;  PRIOR FILING DATE: 2002-06-04
;  PRIOR APPLICATION NUMBER: 60/396,591
;  PRIOR FILING DATE: 2002-07-18
;  PRIOR APPLICATION NUMBER: 60/403,370
;  PRIOR FILING DATE: 2002-08-15
;  PRIOR APPLICATION NUMBER: 60/425,737
;  PRIOR FILING DATE: 2002-11-13
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 76
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; SEQ ID NO 53
;   LENGTH: 243
;   TYPE: PRT
;   ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: CM085C11 scFv
US-10-981-673-53

  Query Match             91.8%;  Score 538;  DB 18;  Length 243;
  Best Local Similarity   91.9%;  Pred. No. 3.5e-42;
  Matches  102;  Conservative    5;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 QSVLTQPPSVSAAPGQKVTISCSGSSSNIGNNFVSWYQQLPGTAPXLLIYDITKRPSGIP 60
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Db        133 QSVLTQPPSVSAAPGQKVTISCSGSTSNIGNNYVSWYQQVPGTAPKLLIYDNNKRPSGIP 192

Qy         61 DRFSGSKSGTSATLGITGLQTGDEADYYCXTWDSSLSAVVFGGGTKLTVLG 111
              |||||||||||||||||||||||||| ||||||||:|||||||:||||
Db        193 DRFSGSKSGTSATLGITGLQTGDEADYYCGTWDSSLSALVFGGGTKVTVLG 243


RESULT 8
US-10-981-691-53
; Sequence 53, Application US/10981691
; Publication No. US20050214208A1
; GENERAL INFORMATION:
;  APPLICANT: Salcedo et al.
;  TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
;  TITLE OF INVENTION:  Receptors
;  FILE REFERENCE: PF585P1D3
;  CURRENT APPLICATION NUMBER: US/10/981,691
;  CURRENT FILING DATE:  2004-11-05
;  PRIOR APPLICATION NUMBER: 60/608,386
;  PRIOR FILING DATE: 2004-09-10
;  PRIOR APPLICATION NUMBER: PCT/US04/013900
;  PRIOR FILING DATE: 2004-05-05
;  PRIOR APPLICATION NUMBER: 60/468,092
;  PRIOR FILING DATE: 2003-05-06
;  PRIOR APPLICATION NUMBER: 60/495,140
;  PRIOR FILING DATE: 2003-08-15
;  PRIOR APPLICATION NUMBER: 10/322,673
;  PRIOR FILING DATE: 2002-12-19
;  PRIOR APPLICATION NUMBER: 60/369,877
;  PRIOR FILING DATE: 2002-04-05
;  PRIOR APPLICATION NUMBER: 60/384,828
;  PRIOR FILING DATE: 2002-06-04
;  PRIOR APPLICATION NUMBER: 60/396,591
;  PRIOR FILING DATE: 2002-07-18
;  PRIOR APPLICATION NUMBER: 60/403,370
;  PRIOR FILING DATE: 2002-08-15
;  PRIOR APPLICATION NUMBER: 60/425,737
;  PRIOR FILING DATE: 2002-11-13
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 76
; SEQ ID NO 53
;   LENGTH: 243
;   TYPE: PRT
;   ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: CM085C11 scFv
US-10-981-691-53

  Query Match             91.8%;  Score 538;  DB 18;  Length 243;
  Best Local Similarity   91.9%;  Pred. No. 3.5e-42;
  Matches  102;  Conservative    5;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 QSVLTQPPSVSAAPGQKVTISCSGSSSNIGNNFVSWYQQLPGTAPXLLIYDITKRPSGIP 60
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Db        133 QSVLTQPPSVSAAPGQKVTISCSGSTSNIGNNYVSWYQQVPGTAPKLLIYDNNKRPSGIP 192

Qy         61 DRFSGSKSGTSATLGITGLQTGDEADYYCXTWDSSLSAVVFGGGTKLTVLG 111
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Db        193 DRFSGSKSGTSATLGITGLQTGDEADYYCGTWDSSLSALVFGGGTKVTVLG 243


RESULT 9
US-10-727-155-309
; Sequence 309, Application US/10727155
; Publication No. US20050049402A1
; GENERAL INFORMATION:
;  APPLICANT: John S. Babcook
;  APPLICANT:  Jaspal S. Kang
;  APPLICANT:  Orit Foord
;  APPLICANT:  Larry Green
;  APPLICANT:  Xiao Feng
;  APPLICANT:  Scott Klakamp
;  APPLICANT:  Mary Haak-Frendscho
;  APPLICANT:  Palaniswami Rathanaswami
;  APPLICANT:  Craig Pigott
;  APPLICANT:  Meina Liang
;  APPLICANT:  Rozanne Lee
;  APPLICANT:  Kathy Manchulencho
;  APPLICANT:  Raffaella Faggioni
;  APPLICANT:  Giorgio Senaldi
;  APPLICANT:  Qiaojuan Jane Su
;  TITLE OF INVENTION: ANTIBODIES DIRECTED TO TUMOR NECROSIS
;  TITLE OF INVENTION:  FACTOR AND USES THEREOF
;  FILE REFERENCE: ABGENIX.073A
;  CURRENT APPLICATION NUMBER: US/10/727,155
;  CURRENT FILING DATE:  2003-12-02
;  PRIOR APPLICATION NUMBER: 60/430729
;  PRIOR FILING DATE: 2002-12-02
;  NUMBER OF SEQ ID NOS: 320
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 309
;   LENGTH: 110
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-727-155-309

  Query Match             91.6%;  Score 537;  DB 17;  Length 110;
  Best Local Similarity   94.5%;  Pred. No. 1.9e-42;
  Matches  104;  Conservative    1;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 QSVLTQPPSVSAAPGQKVTISCSGSSSNIGNNFVSWYQQLPGTAPXLLIYDITKRPSGIP 60
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Db          1 QSVLTQPPSVSAAPGQKVTISCSGSSSNIGNNYVSWYQQLPGTAPKLLIYDNNKRPSGIP 60

Qy         61 DRFSGSKSGTSATLGITGLQTGDEADYYCXTWDSSLSAVVFGGGTKLTVL 110
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Db         61 DRFSGSKSGTSATLGITGLQTGDEADYYCGTWDSSLSAGVFGGGTKLTVL 110


RESULT 10
US-10-727-155-311
; Sequence 311, Application US/10727155
; Publication No. US20050049402A1
; GENERAL INFORMATION:
;  APPLICANT: John S. Babcook
;  APPLICANT:  Jaspal S. Kang
;  APPLICANT:  Orit Foord
;  APPLICANT:  Larry Green
;  APPLICANT:  Xiao Feng
;  APPLICANT:  Scott Klakamp
;  APPLICANT:  Mary Haak-Frendscho
;  APPLICANT:  Palaniswami Rathanaswami
;  APPLICANT:  Craig Pigott
;  APPLICANT:  Meina Liang
;  APPLICANT:  Rozanne Lee
;  APPLICANT:  Kathy Manchulencho
;  APPLICANT:  Raffaella Faggioni
;  APPLICANT:  Giorgio Senaldi
;  APPLICANT:  Qiaojuan Jane Su
;  TITLE OF INVENTION: ANTIBODIES DIRECTED TO TUMOR NECROSIS
;  TITLE OF INVENTION:  FACTOR AND USES THEREOF
;  FILE REFERENCE: ABGENIX.073A
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;  CURRENT APPLICATION NUMBER: US/10/727,155
;  CURRENT FILING DATE:  2003-12-02
;  PRIOR APPLICATION NUMBER: 60/430729
;  PRIOR FILING DATE: 2002-12-02
;  NUMBER OF SEQ ID NOS: 320
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 311
;   LENGTH: 110
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-727-155-311

  Query Match             91.6%;  Score 537;  DB 17;  Length 110;
  Best Local Similarity   94.5%;  Pred. No. 1.9e-42;
  Matches  104;  Conservative    1;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 QSVLTQPPSVSAAPGQKVTISCSGSSSNIGNNFVSWYQQLPGTAPXLLIYDITKRPSGIP 60
              ||||||||||||||||||||||||||||||||:|||||||||||| |||||  |||||||
Db          1 QSVLTQPPSVSAAPGQKVTISCSGSSSNIGNNYVSWYQQLPGTAPKLLIYDNNKRPSGIP 60

Qy         61 DRFSGSKSGTSATLGITGLQTGDEADYYCXTWDSSLSAVVFGGGTKLTVL 110
              ||||||||||||||||||||||||||||| |||||||| ||||||||||
Db         61 DRFSGSKSGTSATLGITGLQTGDEADYYCGTWDSSLSAGVFGGGTKLTVL 110


RESULT 11
US-09-880-748-1260
; Sequence 1260, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
;  APPLICANT: Ruben et al.
;  TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
;  FILE REFERENCE: PF523
;  CURRENT APPLICATION NUMBER: US/09/880,748
;  CURRENT FILING DATE:  2001-06-15
;  PRIOR APPLICATION NUMBER: 60/212,210
;  PRIOR FILING DATE: 2000-06-15
;  PRIOR APPLICATION NUMBER: 60/240,816
;  PRIOR FILING DATE: 2000-10-17
;  PRIOR APPLICATION NUMBER: 60/276,248
;  PRIOR FILING DATE: 2001-03-16
;  PRIOR APPLICATION NUMBER: 60/277,379
;  PRIOR FILING DATE: 2001-03-21
;  PRIOR APPLICATION NUMBER: 60/293,499
;  PRIOR FILING DATE: 2001-05-25
;  NUMBER OF SEQ ID NOS: 3239
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1260
;   LENGTH: 258
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-880-748-1260

  Query Match             91.1%;  Score 534;  DB 10;  Length 258;
  Best Local Similarity   92.8%;  Pred. No. 8.9e-42;
  Matches  103;  Conservative    1;  Mismatches    7;  Indels    0;  Gaps    0;

Qy          1 QSVLTQPPSVSAAPGQKVTISCSGSSSNIGNNFVSWYQQLPGTAPXLLIYDITKRPSGIP 60
              ||||||||||||||||||||||||||||||||:|||||||||||| |||||  |||||||
Db        148 QSVLTQPPSVSAAPGQKVTISCSGSSSNIGNNYVSWYQQLPGTAPKLLIYDNNKRPSGIP 207

Qy         61 DRFSGSKSGTSATLGITGLQTGDEADYYCXTWDSSLSAVVFGGGTKLTVLG 111
              ||||||||||||||||||||||||||||| |||||||| ||| ||||||||
Db        208 DRFSGSKSGTSATLGITGLQTGDEADYYCGAWDSSLSAYVFGSGTKLTVLG 258


RESULT 12
US-10-293-418-1260
; Sequence 1260, Application US/10293418
; Publication No. US20030223996A1
; GENERAL INFORMATION:
;  APPLICANT: Ruben et al.
;  TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
;  FILE REFERENCE: PF523P2
;  CURRENT APPLICATION NUMBER: US/10/293,418
;  CURRENT FILING DATE:  2002-11-27
;  PRIOR APPLICATION NUMBER: 60/331,469
;  PRIOR FILING DATE: 2001-11-16
;  PRIOR APPLICATION NUMBER: 60/340,817
;  PRIOR FILING DATE: 2001-12-19
;  PRIOR APPLICATION NUMBER: 09/880,748
;  PRIOR FILING DATE: 2001-06-15
;  PRIOR APPLICATION NUMBER: 60/293,499
;  PRIOR FILING DATE: 2001-05-25
;  PRIOR APPLICATION NUMBER: 60/277,379
;  PRIOR FILING DATE: 2001-03-21
;  PRIOR APPLICATION NUMBER: 60/276,248
;  PRIOR FILING DATE: 2001-03-16
;  PRIOR APPLICATION NUMBER: 60/240,816
;  PRIOR FILING DATE: 2000-10-17
;  PRIOR APPLICATION NUMBER: 60/212,210
;  PRIOR FILING DATE: 2000-06-16
;  NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1260
;   LENGTH: 258
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-293-418-1260

  Query Match             91.1%;  Score 534;  DB 15;  Length 258;
  Best Local Similarity   92.8%;  Pred. No. 8.9e-42;
  Matches  103;  Conservative    1;  Mismatches    7;  Indels    0;  Gaps    0;

Qy          1 QSVLTQPPSVSAAPGQKVTISCSGSSSNIGNNFVSWYQQLPGTAPXLLIYDITKRPSGIP 60
              ||||||||||||||||||||||||||||||||:|||||||||||| |||||  |||||||
Db        148 QSVLTQPPSVSAAPGQKVTISCSGSSSNIGNNYVSWYQQLPGTAPKLLIYDNNKRPSGIP 207

Qy         61 DRFSGSKSGTSATLGITGLQTGDEADYYCXTWDSSLSAVVFGGGTKLTVLG 111
              ||||||||||||||||||||||||||||| |||||||| ||| ||||||||
Db        208 DRFSGSKSGTSATLGITGLQTGDEADYYCGAWDSSLSAYVFGSGTKLTVLG 258


RESULT 13
US-09-880-748-1246
; Sequence 1246, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
;  APPLICANT: Ruben et al.
;  TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
;  FILE REFERENCE: PF523
;  CURRENT APPLICATION NUMBER: US/09/880,748
;  CURRENT FILING DATE:  2001-06-15
;  PRIOR APPLICATION NUMBER: 60/212,210
;  PRIOR FILING DATE: 2000-06-15
;  PRIOR APPLICATION NUMBER: 60/240,816
;  PRIOR FILING DATE: 2000-10-17
;  PRIOR APPLICATION NUMBER: 60/276,248
;  PRIOR FILING DATE: 2001-03-16
;  PRIOR APPLICATION NUMBER: 60/277,379
;  PRIOR FILING DATE: 2001-03-21
;  PRIOR APPLICATION NUMBER: 60/293,499
;  PRIOR FILING DATE: 2001-05-25
;  NUMBER OF SEQ ID NOS: 3239
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1246
;   LENGTH: 248
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-880-748-1246

  Query Match             91.0%;  Score 533;  DB 10;  Length 248;
  Best Local Similarity   93.7%;  Pred. No. 1.1e-41;
  Matches  104;  Conservative    1;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 QSVLTQPPSVSAAPGQKVTISCSGSSSNIGNNFVSWYQQLPGTAPXLLIYDITKRPSGIP 60
              |||||||||||||||||||||||||||||||| |||||||||||| |||||  |||||||
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Db        138 QSVLTQPPSVSAAPGQKVTISCSGSSSNIGNNNVSWYQQLPGTAPKLLIYDNNKRPSGIP 197

Qy         61 DRFSGSKSGTSATLGITGLQTGDEADYYCXTWDSSLSAVVFGGGTKLTVLG 111
              ||||||||||||||||||||||||||:| |||||| ||||||||||||||
Db        198 DRFSGSKSGTSATLGITGLQTGDEADYHCGTWDSSLVAVVFGGGTKLTVLG 248
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RESULT 14
US-10-293-418-1246
; Sequence 1246, Application US/10293418
; Publication No. US20030223996A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
; FILE REFERENCE: PF523P2
; CURRENT APPLICATION NUMBER: US/10/293,418
; CURRENT FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1246
; LENGTH: 248
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-418-1246

Query Match 91.0%; Score 533; DB 15; Length 248;
Best Local Similarity 93.7%; Pred. No. 1.1e-41;
Matches 104; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

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Qy          1 QSVLTQPPSVSAAPGQKVTISCSGSSSNIGNNFVSWYQQLPGTAPXLLIYDITKRPSGIP 60
              |||||||||||||||||||||||||||||| |||||||||||| ||||| |||||||
Db        138 QSVLTQPPSVSAAPGQKVTISCSGSSSNIGNNNVSWYQQLPGTAPKLLIYDNNKRPSGIP 197

Qy         61 DRFSGSKSGTSATLGITGLQTGDEADYYCXTWDSSLSAVVFGGGTKLTVLG 111
              ||||||||||||||||||||||||||:| |||||| ||||||||||||||
Db        198 DRFSGSKSGTSATLGITGLQTGDEADYHCGTWDSSLVAVVFGGGTKLTVLG 248
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RESULT 15
US-10-269-805-10
; Sequence 10, Application US/10269805
; Publication No. US20030124129A1
; GENERAL INFORMATION:
; APPLICANT: OLINER, JONATHAN D.
; TITLE OF INVENTION: ANGIOPOIETIN-2 SPECIFIC BINDING AGENTS
; FILE REFERENCE: A-722
; CURRENT APPLICATION NUMBER: US/10/269,805
; CURRENT FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: US 60/328,604
; PRIOR FILING DATE: 2001-10-11
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-269-805-10

Query Match 90.8%; Score 532; DB 14; Length 112;
Best Local Similarity 92.9%; Pred. No. 5.7e-42;
Matches 104; Conservative 2; Mismatches 4; Indels 2; Gaps 1;

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Qy          1 QSVLTQPPSVSAAPGQKVTISCSGSSSNIGNNFVSWYQQLPGTAPXLLIYDITKRPSGIP 60
              |||||||||||||||||||||||:|||||||||||||||||||| ||:|| |||||||
Db          1 QSVLTQPPSVSAAPGQKVTISCSGSNSNIGNNFVSWYQQLPGTAPKLLVYDNNKRPSGIP 60

Qy         61 DRFSGSKSGTSATLGITGLQTGDEADYYCXTWDSSLSA--VVFGGGTKLTVL 110
              |||||||||||||||||||||||||||||| |||||||| ||||||||||
Db         61 DRFSGSKSGTSATLGITGLQTGDEADYYCGTWDSSLSAAEVVFGGGTKLTVL 112
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Job time : 111.575 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: October 13, 2005, 02:37:04 ; Search time 18.5923 Seconds
(without alignments)
457.717 Million cell updates/sec

Title: US-10-010-729A-9
Perfect score: 586
Sequence: 1 QSVLTQPPSVSAAPGQKVTI.....SLSAVVPGGGTKLTVLGQPK 114

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	544	92.8	234	4	US-09-372-425A-4	Sequence 4, Appli
2	518	88.4	112	3	US-09-025-769B-18	Sequence 18, Appl
3	518	88.4	112	4	US-09-490-070A-18	Sequence 18, Appl
4	518	88.4	112	4	US-09-490-153-18	Sequence 18, Appl
5	518	88.4	112	4	US-09-490-324-18	Sequence 18, Appl
6	515	87.9	110	1	US-08-199-911-2	Sequence 2, Appli
7	515	87.9	114	3	US-09-240-274-62	Sequence 62, Appl
8	513.5	87.6	112	3	US-08-983-607-31	Sequence 31, Appl
9	494.5	84.4	132	2	US-08-345-321-4	Sequence 4, Appli
10	493	84.1	109	3	US-09-240-274-61	Sequence 61, Appl
11	486	82.9	111	2	US-08-665-202-36	Sequence 36, Appl
12	486	82.9	111	4	US-09-315-574-36	Sequence 36, Appl
13	486	82.9	258	2	US-08-665-202-5	Sequence 5, Appli
14	486	82.9	258	4	US-09-315-574-5	Sequence 5, Appli
15	486	82.9	262	3	US-09-069-821-4	Sequence 4, Appli
16	486	82.9	262	4	US-09-956-086-4	Sequence 4, Appli
17	486	82.9	262	4	US-09-956-087-4	Sequence 4, Appli
18	486	82.9	282	3	US-09-420-592A-7	Sequence 7, Appli
19	486	82.9	282	4	US-09-985-442-7	Sequence 7, Appli
20	486	82.9	282	4	US-09-983-580-7	Sequence 7, Appli
21	485	82.8	111	2	US-08-665-202-42	Sequence 42, Appl
22	485	82.8	111	4	US-09-315-574-42	Sequence 42, Appl
23	484	82.6	98	2	US-08-665-202-37	Sequence 37, Appl
24	484	82.6	98	4	US-09-315-574-37	Sequence 37, Appl
25	484	82.6	111	2	US-08-665-202-43	Sequence 43, Appl
26	484	82.6	111	4	US-09-315-574-43	Sequence 43, Appl
27	482	82.3	111	3	US-08-983-607-35	Sequence 35, Appl
28	480	81.9	111	2	US-08-665-202-40	Sequence 40, Appl
29	480	81.9	111	4	US-09-315-574-40	Sequence 40, Appl
30	479.5	81.8	112	2	US-08-665-202-39	Sequence 39, Appl
31	479.5	81.8	112	4	US-09-315-574-39	Sequence 39, Appl
32	479	81.7	236	3	US-08-487-550-10	Sequence 10, Appl
33	479	81.7	236	4	US-09-526-098-10	Sequence 10, Appl
34	479	81.7	236	4	US-09-383-916-10	Sequence 10, Appl
35	474.5	81.0	236	3	US-09-049-672A-7	Sequence 7, Appli
36	466	79.5	113	1	US-08-211-202-112	Sequence 112, App
37	463	79.0	111	4	US-09-424-840B-8	Sequence 8, Appli
38	454	77.5	109	3	US-09-240-274-54	Sequence 54, Appl
39	454	77.5	111	1	US-08-264-093-6	Sequence 6, Appli
40	454	77.5	111	2	US-08-665-202-41	Sequence 41, Appl
41	454	77.5	111	4	US-09-315-574-41	Sequence 41, Appl
42	450	76.8	111	2	US-08-652-816A-15	Sequence 15, Appl
43	450	76.8	113	1	US-08-211-202-113	Sequence 113, App
44	448	76.5	109	3	US-09-025-769B-32	Sequence 32, Appl
45	448	76.5	109	3	US-09-025-769B-51	Sequence 51, Appl

ALIGNMENTS

RESULT 1
US-09-372-425A-4
; Sequence 4, Application US/09372425A
; Patent No. 6475749
; GENERAL INFORMATION:
; APPLICANT: Sherie L. Morrison
; APPLICANT: Ramon Montano
; TITLE OF INVENTION: Improved Rh Antibody
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Oppenheimer Wolff & Donnelly LLP
; STREET: 2029 Century Park East, Suite 3800
; CITY: Los Angeles
; STATE: CA
; COUNTRY: USA
; ZIP: 90067
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 98
; SOFTWARE: MS Word
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/372,425A
; FILING DATE: August 11, 1999
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Oldenakmp, David J.
; REGISTRATION NUMBER: 29,421
; REFERENCE/DOCKET NUMBER: 510015-223
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (310) 788-5000
; TELEFAX: (310) 788-5100
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 234 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Light chain - AA
US-09-372-425A-4

Query Match 92.8%; Score 544; DB 4; Length 234;
Best Local Similarity 90.4%; Pred. No. 4.1e-46;
Matches 103; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

Qy 1 QSVLTQPPSVSAAPGQKVTISCSGSSSNIGNNFVSWYQQLPGTAPXLLIYDITKRPSGIP 60

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Db         19 QSVLTQPPSVSAAPGQKVTISCSGSSSNIGNNYVSWYQHFPGTAPKLLIYDNNQRPSGIP 78

Qy         61 DRFSGSKSGTSATLGITGLQTGDEADYYCXTWDSSLSAVVFGGGTKLTVLGQPK 114
              |||||||||||||||||||||||||||||| |||||||||:|||||::|||||||
Db         79 DRFSGSKSGTSATLGITGLQTGDEADYYCGTWDSSLSAVLFGGGTEVTVLGQPK 132


RESULT 2
US-09-025-769B-18
; Sequence 18, Application US/09025769B
; Patent No. 6300064
;  GENERAL INFORMATION:
;    APPLICANT:  Knappik, Achim
;    APPLICANT:  Pack, Peter
;    APPLICANT:  Ilag, Vic
;    APPLICANT:  Ge, Liming
;    APPLICANT:  Moroney, Simon
;    APPLICANT:  Plueckthun, Andreas
;    TITLE OF INVENTION:  Protein/(Poly)peptide libraries
;    NUMBER OF SEQUENCES:  373
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  James F. Haley, Jr., Esq. c/o Fish & Neave
;      STREET:  1251 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  USA
;      ZIP:  10021
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30 (EPO)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/025,769B
;      FILING DATE:  18-FEB-1998
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  EP 95 11 3021.0
;      FILING DATE:  18-AUG-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  James F. Haley, Jr., Esq.
;      REGISTRATION NUMBER:  27,794
;      REFERENCE/DOCKET NUMBER:  MORPHO/5
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212)596-9000
;      TELEFAX:  (212)596-9090
;  INFORMATION FOR SEQ ID NO:  18:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  112 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-09-025-769B-18

  Query Match             88.4%;  Score 518;  DB 3;  Length 112;
  Best Local Similarity   87.5%;  Pred. No. 6.4e-44;
  Matches   98;  Conservative    5;  Mismatches    9;  Indels    0;  Gaps    0;

Qy          1 QSVLTQPPSVSAAPGQKVTISCSGSSSNIGNNFVSWYQQLPGTAPXLLIYDITKRPSGIP 60
              |||||||||||| ||||:|||||||||||||||:|||||||||||| |||||  |||||:|
Db          1 QSVLTQPPSVSGAPGQRVTISCSGSSSNIGNNYVSWYQQLPGTAPKLLIYDNNKRPSGVP 60

Qy         61 DRFSGSKSGTSATLGITGLQTGDEADYYCXTWDSSLSAVVFGGGTKLTVLGQ 112
              |||||||||||:| |||||: ||||||| ||| ||| ||||||||||||||
Db         61 DRFSGSKSGTSASLAITGLQSEDEADYYCATWDDSLSGVVFGGGTKLTVLGQ 112


RESULT 3
US-09-490-070A-18
; Sequence 18, Application US/09490070A
; Patent No. 6696248
;   GENERAL INFORMATION:
;        APPLICANT: Knappik, Achim
;                   Pack, Peter
;                   Ilag, Vic
;                   Ge, Liming
;                   Moroney, Simon
;                   Plueckthun, Andreas
;        TITLE OF INVENTION: Protein/(Poly)peptide libraries
;        NUMBER OF SEQUENCES: 373
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Colin G. Sandercock, Esq. c/o Heller Ehrman
;                        White & McAuliffe
;             STREET: 1666 K Street, N.W., Suite 300
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20006
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/490,070A
;             FILING DATE: 24-Jan-2000
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: EP 95 11 3021.0
;             FILING DATE: 18-AUG-1995
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Colin G. Sandercock, Esq.
;             REGISTRATION NUMBER: 31,298
;             REFERENCE/DOCKET NUMBER: 37629-0005
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (202) 912-2000
;             TELEFAX: (202) 912-2020
;   INFORMATION FOR SEQ ID NO: 18:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 112 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: <Unknown>
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-09-490-070A-18

  Query Match             88.4%;  Score 518;  DB 4;  Length 112;
  Best Local Similarity   87.5%;  Pred. No. 6.4e-44;
  Matches   98;  Conservative    5;  Mismatches    9;  Indels    0;  Gaps    0;

Qy          1 QSVLTQPPSVSAAPGQKVTISCSGSSSNIGNNFVSWYQQLPGTAPXLLIYDITKRPSGIP 60
              |||||||||||| ||||:|||||||||||||||:|||||||||||| |||||  |||||:|
Db          1 QSVLTQPPSVSGAPGQRVTISCSGSSSNIGNNYVSWYQQLPGTAPKLLIYDNNKRPSGVP 60

Qy         61 DRFSGSKSGTSATLGITGLQTGDEADYYCXTWDSSLSAVVFGGGTKLTVLGQ 112
              |||||||||||:| |||||: ||||||| ||| ||| ||||||||||||||
Db         61 DRFSGSKSGTSASLAITGLQSEDEADYYCATWDDSLSGVVFGGGTKLTVLGQ 112


RESULT 4
US-09-490-153-18
; Sequence 18, Application US/09490153
; Patent No. 6706484
;   GENERAL INFORMATION:
;        APPLICANT: Knappik, Achim
;                   Pack, Peter
;                   Ilag, Vic
;                   Ge, Liming
;                   Moroney, Simon
;                   Plueckthun, Andreas
;        TITLE OF INVENTION: Protein/(Poly)peptide libraries
;        NUMBER OF SEQUENCES: 373
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
;             STREET: 1251 Avenue of the Americas
;             CITY: New York
```

```
;              STATE: New York
;              COUNTRY: USA
;              ZIP: 10021
;         COMPUTER READABLE FORM:
;              MEDIUM TYPE: Floppy disk
;              COMPUTER: IBM PC compatible
;              OPERATING SYSTEM: PC-DOS/MS-DOS
;              SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
;         CURRENT APPLICATION DATA:
;              APPLICATION NUMBER: US/09/490,153
;              FILING DATE: 24-Jan-2000
;         PRIOR APPLICATION DATA:
;              APPLICATION NUMBER: US/09/025,769B
;              FILING DATE: 18-FEB-1998
;              APPLICATION NUMBER: EP 95 11 3021.0
;              FILING DATE: 18-AUG-1995
;         ATTORNEY/AGENT INFORMATION:
;              NAME: James F. Haley, Jr., Esq.
;              REGISTRATION NUMBER: 27,794
;              REFERENCE/DOCKET NUMBER: MORPHO/5
;         TELECOMMUNICATION INFORMATION:
;              TELEPHONE: (212)596-9000
;              TELEFAX: (212)596-9090
;    INFORMATION FOR SEQ ID NO: 18:
;         SEQUENCE CHARACTERISTICS:
;              LENGTH: 112 amino acids
;              TYPE: amino acid
;              STRANDEDNESS: <Unknown>
;              TOPOLOGY: linear
;         MOLECULE TYPE: protein
;         SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-09-490-153-18

  Query Match             88.4%;  Score 518;  DB 4;  Length 112;
  Best Local Similarity   87.5%;  Pred. No. 6.4e-44;
  Matches   98;  Conservative    5;  Mismatches    9;  Indels    0;  Gaps    0;

Qy          1 QSVLTQPPSVSAAPGQKVTISCSGSSSNIGNNFVSWYQQLPGTAPXLLIYDITKRPSGIP 60
              ||||||||||| ||||:|||||||||||||||:|||||||||||| |||||  |||||:|
Db          1 QSVLTQPPSVSGAPGQRVTISCSGSSSNIGNNYVSWYQQLPGTAPKLLIYDNNKRPSGVP 60

Qy         61 DRFSGSKSGTSATLGITGLQTGDEADYYCXTWDSSLSAVVFGGGTKLTVLGQ 112
              ||||||||||||:| |||||: ||||||| ||| ||| ||||||||||||||
Db         61 DRFSGSKSGTSASLAITGLQSEDEADYYCATWDDSLSGVVFGGGTKLTVLGQ 112


RESULT 5
US-09-490-324-18
; Sequence 18, Application US/09490324
; Patent No. 6828422
;   GENERAL INFORMATION:
;         APPLICANT: Knappik, Achim
;                    Pack, Peter
;                    Ilag, Vic
;                    Ge, Liming
;                    Moroney, Simon
;                    Plueckthun, Andreas
;         TITLE OF INVENTION: Protein/(Poly)peptide libraries
;         NUMBER OF SEQUENCES: 373
;         CORRESPONDENCE ADDRESS:
;              ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
;              STREET: 1251 Avenue of the Americas
;              CITY: New York
;              STATE: New York
;              COUNTRY: USA
;              ZIP: 10021
;         COMPUTER READABLE FORM:
;              MEDIUM TYPE: Floppy disk
;              COMPUTER: IBM PC compatible
;              OPERATING SYSTEM: PC-DOS/MS-DOS
;              SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
;         CURRENT APPLICATION DATA:
;              APPLICATION NUMBER: US/09/490,324
;              FILING DATE: 24-Jan-2000
;         PRIOR APPLICATION DATA:
;              APPLICATION NUMBER: US/09/025,769
;              FILING DATE: 18-FEB-1998
;              APPLICATION NUMBER: EP 95 11 3021.0
;              FILING DATE: 18-AUG-1995
;         ATTORNEY/AGENT INFORMATION:
;              NAME: James F. Haley, Jr., Esq.
;              REGISTRATION NUMBER: 27,794
;              REFERENCE/DOCKET NUMBER: MORPHO/5
;         TELECOMMUNICATION INFORMATION:
;              TELEPHONE: (212)596-9000
;              TELEFAX: (212)596-9090
;    INFORMATION FOR SEQ ID NO: 18:
;         SEQUENCE CHARACTERISTICS:
;              LENGTH: 112 amino acids
;              TYPE: amino acid
;              STRANDEDNESS: <Unknown>
;              TOPOLOGY: linear
;         MOLECULE TYPE: protein
;         SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-09-490-324-18

  Query Match             88.4%;  Score 518;  DB 4;  Length 112;
  Best Local Similarity   87.5%;  Pred. No. 6.4e-44;
  Matches   98;  Conservative    5;  Mismatches    9;  Indels    0;  Gaps    0;

Qy          1 QSVLTQPPSVSAAPGQKVTISCSGSSSNIGNNFVSWYQQLPGTAPXLLIYDITKRPSGIP 60
              ||||||||||| ||||:|||||||||||||||:|||||||||||| |||||  |||||:|
Db          1 QSVLTQPPSVSGAPGQRVTISCSGSSSNIGNNYVSWYQQLPGTAPKLLIYDNNKRPSGVP 60

Qy         61 DRFSGSKSGTSATLGITGLQTGDEADYYCXTWDSSLSAVVFGGGTKLTVLGQ 112
              ||||||||||||:| |||||: ||||||| ||| ||| ||||||||||||||
Db         61 DRFSGSKSGTSASLAITGLQSEDEADYYCATWDDSLSGVVFGGGTKLTVLGQ 112


RESULT 6
US-08-199-911-2
; Sequence 2, Application US/08199911
; Patent No. 5495002
;  GENERAL INFORMATION:
;    APPLICANT:  Kobrin, Barry J.
;    APPLICANT:  Haspel, Martin V.
;    TITLE OF INVENTION:  Tumor Associated Monoclonal Antibody
;    TITLE OF INVENTION:  123AV16
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  AKZO NOBEL
;      STREET:  1330 Piccard Drive
;      CITY:  Rockville
;      STATE:  Maryland
;      COUNTRY:  USA
;      ZIP:  20850
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/199,911
;      FILING DATE:  22-FEB-1994
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/065,517
;      FILING DATE:  21-MAY-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/636,179
;      FILING DATE:  31-DEC-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/302,155
;      FILING DATE:  25-JAN-1989
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 06/697,078
```

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;      FILING DATE:  31-JAN-1985
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 06/575,533
;      FILING DATE:  31-JAN-1984
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Gormley, Mary E.
;      REGISTRATION NUMBER:  34,409
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  301-258-5200
;      TELEFAX:  301-977-0847
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  110 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-199-911-2

  Query Match             87.9%;  Score 515;  DB 1;  Length 110;
  Best Local Similarity   89.1%;  Pred. No. 1.2e-43;
  Matches   98;  Conservative    3;  Mismatches    9;  Indels    0;  Gaps    0;

Qy          1 QSVLTQPPSVSAAPGQKVTISCSGSSSNIGNNFVSWYQQLPGTAPXLLIYDITKRPSGIP 60
              || |||||||||||||||||||||:||||||||||||| ||||| |||||  |||||:|
Db          1 QSALTQPPSVSAAPGQKVTISCSGTSSNIGNNFVSWYQQFPGTAPKLLIYDNNKRPSGVP 60

Qy         61 DRFSGSKSGTSATLGITGLQTGDEADYYCXTWDSSLSAVVFGGGTKLTVL 110
              |||||||||||||||||||||||||||| |||: | | ||||||||||
Db         61 DRFSGSKSGTSATLGITGLQTGDEADYYCGTWDTRLRAGVFGGGTKLTVL 110


RESULT 7
US-09-240-274-62
; Sequence 62, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
;  APPLICANT: Siegel, Donald L.
;  TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
;  TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
;  FILE REFERENCE: 09596-42U2
;  CURRENT APPLICATION NUMBER: US/09/240,274
;  CURRENT FILING DATE: 1999-01-29
;  EARLIER APPLICATION NUMBER: 60/081,380
;  EARLIER FILING DATE: 1998-04-10
;  EARLIER APPLICATION NUMBER: 60/028,550
;  EARLIER FILING DATE: 1996-10-11
;  NUMBER OF SEQ ID NOS: 224
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 62
;   LENGTH: 114
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: anti-Rh(D) chain N02
US-09-240-274-62

  Query Match             87.9%;  Score 515;  DB 3;  Length 114;
  Best Local Similarity   90.2%;  Pred. No. 1.3e-43;
  Matches  101;  Conservative    2;  Mismatches    5;  Indels    4;  Gaps    1;

Qy          4 LTQPPSVSAAPGQKVTISCSGSSSNIGNNFVSWYQQLPGTAPXLLIYDITKRPSGIPDRF 63
              |||||||||||||||||||||||||||||:|||||||||||| |||||  ||||||||||
Db          3 LTQPPSVSAAPGQKVTISCSGSSSNIGNNYVSWYQQLPGTAPKLLIYDNNKRPSGIPDRF 62

Qy         64 SGSKSGTSATLGITGLQTGDEADYYCXTWDSSLSA----VVFGGGTKLTVLG 111
              |||||||||||||||||||||||||| ||||||||     :||||||||||
Db         63 SGSKSGTSATLGITGLQTGDEADYYCGTWDSSLSAGRVRRMFGGGTKLTVLG 114


RESULT 8
US-08-983-607-31
; Sequence 31, Application US/08983607
; Patent No. 6140470
;  GENERAL INFORMATION:
;    APPLICANT:  Alan Garen
;    APPLICANT:  Xiaohong Cai
;    TITLE OF INVENTION:  Human Anti-Tumor Monoclonal Anti-
;    TITLE OF INVENTION:  bodies
;    NUMBER OF SEQUENCES:  51
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Department of Molecular Biophysics
;      ADDRESSEE:  and Biochemistry, Yale University
;      STREET:  266 Whitney Avenue
;      CITY:  New Haven
;      STATE:  Connecticut
;      COUNTRY:  United States of America
;      ZIP:  06520-8114
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" 1.44 Mb diskette
;      COMPUTER:  IBM PC
;      OPERATING SYSTEM:  MS DOS
;      SOFTWARE:  Word Processing
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/983,607
;      FILING DATE:  April 27, 1998
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/IB96/01032
;      FILING DATE:  June 28, 1996
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Mary M. Krinsky
;      REGISTRATION NUMBER:  32423
;      REFERENCE/DOCKET NUMBER:  OCR-679
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  203-773-9544
;      TELEFAX:  203-773-1183
;  INFORMATION FOR SEQ ID NO:  31:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  112 residues
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:
;      DESCRIPTION:  polypeptide
;    ORIGINAL SOURCE:
;      ORGANISM:  Homo sapiens (melanoma patient immu-
;      ORGANISM:  nized with autologous tumor cells)
;      INDIVIDUAL ISOLATE:  peripheral blood lymphocytes
;    IMMEDIATE SOURCE:
;      LIBRARY:  DM414 scFv antibodies obtained from
;      LIBRARY:  fUSE5 fusion phage construct
;      CLONE:  V73
;    FEATURE:
;      NAME/KEY:  light chain
US-08-983-607-31

  Query Match             87.6%;  Score 513.5;  DB 3;  Length 112;
  Best Local Similarity   90.2%;  Pred. No. 1.8e-43;
  Matches  101;  Conservative    3;  Mismatches    7;  Indels    1;  Gaps    1;

Qy          1 QSVLTQPPSVSAAPGQKVT-ISCSGSSSNIGNNFVSWYQQLPGTAPXLLIYDITKRPSGI 59
              || |||||||||||||||| ||||||||||||:|||||||||||| ||||:  ||||||
Db          1 QSALTQPPSVSAAPGQKVTXISCSGSSSNIGNNYVSWYQQLPGTAPKLLIYENNKRPSGI 60

Qy         60 PDRFSGSKSGTSATLGITGLQTGDEADYYCXTWDSSLSAVVFGGGTKLTVLG 111
              |||||||||||||||||||||||||||||| |||||||| ||| ||:|||||
Db         61 PDRFSGSKSGTSATLGITGLQTGDEADYYCGTWDSSLSAEVFGTGTQLTVLG 112


RESULT 9
US-08-345-321-4
; Sequence 4, Application US/08345321
; Patent No. 5914109
;  GENERAL INFORMATION:
;    APPLICANT:  ZOLLA-PAZNER, Susan
```

```
;    APPLICANT:  GORNY, Miroslav K.
;    TITLE OF INVENTION:  HETEROHYBRIDOMAS PRODUCING HUMAN
;    TITLE OF INVENTION:  MONOCLONAL ANTIBODIES TO HIV-1
;    NUMBER OF SEQUENCES:  22
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Browdy and Neimark
;      STREET:  419 Seventh Street, N.W., Suite 300
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20004
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/345,321
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/872,675
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Browdy, Roger L.
;      REGISTRATION NUMBER:  25,618
;      REFERENCE/DOCKET NUMBER:  ZOLLA-PAZNER1B
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-628-5197
;      TELEFAX:  202-737-3528
;      TELEX:  248633
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  132 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-345-321-4

  Query Match             84.4%;  Score 494.5;  DB 2;  Length 132;
  Best Local Similarity   88.3%;  Pred. No. 1.6e-41;
  Matches   98;  Conservative    2;  Mismatches   10;  Indels    1;  Gaps    1;

Qy          1 QSVLTQPPSVSAAPGQKVTISCSGSSSNIGNNFVSWYQQLPGTAPXLLIYDITKRPSGIP 60
              ||||||||||||||||||||||||||||| ||:| |||| ||||| ||||    |||||||
Db         20 QSVLTQPPSVSAAPGQKVTISCSGSSSNIPNNYVLWYQQFPGTAPKLLIYGNNKRPSGIP 79

Qy         61 DRFSGSKSGTSATLGITGLQTGDEADYYCXTWDSSLSA-VVFGGGTKLTVL 110
              |||||||||||||||||||||||||||:| |||| |||  ||||||||||
Db         80 DRFSGSKSGTSATLGITGLQTGDEADYFCATWDSGLSADWVFGGGTKLTVL 130


RESULT 10
US-09-240-274-61
; Sequence 61, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
;  APPLICANT: Siegel, Donald L.
;  TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
;  TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
;  FILE REFERENCE: 09596-42U2
;  CURRENT APPLICATION NUMBER: US/09/240,274
;  CURRENT FILING DATE: 1999-01-29
;  EARLIER APPLICATION NUMBER: 60/081,380
;  EARLIER FILING DATE: 1998-04-10
;  EARLIER APPLICATION NUMBER: 60/028,550
;  EARLIER FILING DATE: 1996-10-11
;  NUMBER OF SEQ ID NOS: 224
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 61
;   LENGTH: 109
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: anti-Rh(D) chain N01
US-09-240-274-61

  Query Match             84.1%;  Score 493;  DB 3;  Length 109;
  Best Local Similarity   87.9%;  Pred. No. 1.8e-41;
  Matches   94;  Conservative    5;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          4 LTQPPSVSAAPGQKVTISCSGSSSNIGNNFVSWYQQLPGTAPXLLIYDITKRPSGIPDRF 63
              ||||||||||||||||||||||||||| :|:|||||||||||| |||:|  :|||||||||
Db          3 LTQPPSVSAAPGQKVTISCSGSSSNIDSNYVSWYQQLPGTAPKLLIFDNYRRPSGIPDRF 62

Qy         64 SGSKSGTSATLGITGLQTGDEADYYCXTWDSSLSAVVFGGGTKLTVL 110
              ||||||||||||||||||||||||||| ||| ||:  ||||||||||
Db         63 SGSKSGTSATLGITGLQTGDEADYYCATWDDSLNGRVFGGGTKLTVL 109


RESULT 11
US-08-665-202-36
; Sequence 36, Application US/08665202
; Patent No. 5977322
; GENERAL INFORMATION:
;    APPLICANT:  Marks, James D.
;    APPLICANT:  Schier, Robert
;    TITLE OF INVENTION:  No. 5977322el High Affinity Human Antibodies to
;    TITLE OF INVENTION:  Tumor Antigens
;    NUMBER OF SEQUENCES:  141
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend and Crew LLP
;      STREET:  Two Embarcadero Center, Eighth Floor
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94111-3834
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/665,202
;      FILING DATE:  13-JUN-1996
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/000,238
;      FILING DATE:  14-JUN-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/000,250
;      FILING DATE:  15-JUN-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Hunter, Tom
;      REGISTRATION NUMBER:  38,498
;      REFERENCE/DOCKET NUMBER:  02307E-061410
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 576-0200
;      TELEFAX:  (415) 576-0300
;  INFORMATION FOR SEQ ID NO:  36:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  111 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-665-202-36

  Query Match             82.9%;  Score 486;  DB 2;  Length 111;
  Best Local Similarity   82.9%;  Pred. No. 9.1e-41;
  Matches   92;  Conservative    7;  Mismatches   12;  Indels    0;  Gaps    0;

Qy          1 QSVLTQPPSVSAAPGQKVTISCSGSSSNIGNNFVSWYQQLPGTAPXLLIYDITKRPSGIP 60
              |||||||||||||||||||||||||||||:|||||||||||| |||| | ||:|:|
Db          1 QSVLTQPPSVSAAPGQKVTISCSGSSSNIGNNYVSWYQQLPGTAPKLLIYGHTNRPAGVP 60
```

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Qy          61 DRFSGSKSGTSATLGITGLQTGDEADYYCXTWDSSLSAVVFGGGTKLTVLG 111
               ||||||||||||:| |:| :: ||||||| || ||| ||||||||||||
Db          61 DRFSGSKSGTSASLAISGFRSEDEADYYCAAWDDSLSGWVFGGGTKLTVLG 111


RESULT 12
US-09-315-574-36
; Sequence 36, Application US/09315574
; Patent No. 6512097
;  GENERAL INFORMATION:
;    APPLICANT:  Marks, James D.
;    APPLICANT:  Schier, Robert
;    TITLE OF INVENTION:  No. 6512097el High Affinity Human Antibodies to
;    TITLE OF INVENTION:  Tumor Antigens
;    NUMBER OF SEQUENCES:  141
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Majestic, Parsons, Siebert & Hsue P.C.
;      STREET:  Four Embarcadero Center, Suite 1100
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94111-4106
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/315,574
;      FILING DATE:  20-MAY-99
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/000,238
;      FILING DATE:  14-JUN-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/000,250
;      FILING DATE:  15-JUN-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/665,202
;      FILING DATE:  13-JUN-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Hunter, Tom
;      REGISTRATION NUMBER:  38,498
;      REFERENCE/DOCKET NUMBER:  02307E-061411
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 576-0200
;      TELEFAX:  (415) 576-0300
;  INFORMATION FOR SEQ ID NO:  36:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  111 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-09-315-574-36

  Query Match             82.9%;  Score 486;  DB 4;  Length 111;
  Best Local Similarity   82.9%;  Pred. No. 9.1e-41;
  Matches   92;  Conservative    7;  Mismatches   12;  Indels    0;  Gaps    0;

Qy           1 QSVLTQPPSVSAAPGQKVTISCSGSSSNIGNNFVSWYQQLPGTAPXLLIYDITKRPSGIP 60
               |||||||||||||||||||||||||||||:|||||||||||| |||| | ||:|:|
Db           1 QSVLTQPPSVSAAPGQKVTISCSGSSSNIGNNYVSWYQQLPGTAPKLLIYGHTNRPAGVP 60

Qy          61 DRFSGSKSGTSATLGITGLQTGDEADYYCXTWDSSLSAVVFGGGTKLTVLG 111
               ||||||||||||:| |:| :: ||||||| || ||| ||||||||||||
Db          61 DRFSGSKSGTSASLAISGFRSEDEADYYCAAWDDSLSGWVFGGGTKLTVLG 111


RESULT 13
US-08-665-202-5
; Sequence 5, Application US/08665202
; Patent No. 5977322
;  GENERAL INFORMATION:
;    APPLICANT:  Marks, James D.
;    APPLICANT:  Schier, Robert
;    TITLE OF INVENTION:  No. 5977322el High Affinity Human Antibodies to
;    TITLE OF INVENTION:  Tumor Antigens
;    NUMBER OF SEQUENCES:  141
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend and Crew LLP
;      STREET:  Two Embarcadero Center, Eighth Floor
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94111-3834
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/665,202
;      FILING DATE:  13-JUN-1996
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/000,238
;      FILING DATE:  14-JUN-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/000,250
;      FILING DATE:  15-JUN-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Hunter, Tom
;      REGISTRATION NUMBER:  38,498
;      REFERENCE/DOCKET NUMBER:  02307E-061410
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 576-0200
;      TELEFAX:  (415) 576-0300
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  258 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-665-202-5

  Query Match             82.9%;  Score 486;  DB 2;  Length 258;
  Best Local Similarity   82.9%;  Pred. No. 2.4e-40;
  Matches   92;  Conservative    7;  Mismatches   12;  Indels    0;  Gaps    0;

Qy           1 QSVLTQPPSVSAAPGQKVTISCSGSSSNIGNNFVSWYQQLPGTAPXLLIYDITKRPSGIP 60
               |||||||||||||||||||||||||||||:|||||||||||| |||| | ||:|:|
Db         145 QSVLTQPPSVSAAPGQKVTISCSGSSSNIGNNYVSWYQQLPGTAPKLLIYGHTNRPAGVP 204

Qy          61 DRFSGSKSGTSATLGITGLQTGDEADYYCXTWDSSLSAVVFGGGTKLTVLG 111
               ||||||||||||:| |:| :: ||||||| || ||| ||||||||||||
Db         205 DRFSGSKSGTSASLAISGFRSEDEADYYCAAWDDSLSGWVFGGGTKLTVLG 255


RESULT 14
US-09-315-574-5
; Sequence 5, Application US/09315574
; Patent No. 6512097
;  GENERAL INFORMATION:
;    APPLICANT:  Marks, James D.
;    APPLICANT:  Schier, Robert
;    TITLE OF INVENTION:  No. 6512097el High Affinity Human Antibodies to
;    TITLE OF INVENTION:  Tumor Antigens
;    NUMBER OF SEQUENCES:  141
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Majestic, Parsons, Siebert & Hsue P.C.
;      STREET:  Four Embarcadero Center, Suite 1100
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94111-4106
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;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.30
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/09/315,574
;       FILING DATE:  20-MAY-99
;       CLASSIFICATION:  530
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 60/000,238
;       FILING DATE:  14-JUN-1995
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 60/000,250
;       FILING DATE:  15-JUN-1995
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 08/665,202
;       FILING DATE:  13-JUN-1996
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Hunter, Tom
;       REGISTRATION NUMBER:  38,498
;       REFERENCE/DOCKET NUMBER:  02307E-061411
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (415) 576-0200
;       TELEFAX:  (415) 576-0300
;   INFORMATION FOR SEQ ID NO:  5:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  258 amino acids
;       TYPE:  amino acid
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  protein
US-09-315-574-5

  Query Match             82.9%;  Score 486;  DB 4;  Length 258;
  Best Local Similarity   82.9%;  Pred. No. 2.4e-40;
  Matches   92;  Conservative    7;  Mismatches   12;  Indels    0;  Gaps    0;

Qy          1 QSVLTQPPSVSAAPGQKVTISCSGSSSNIGNNFVSWYQQLPGTAPXLLIYDITKRPSGIP 60
              ||||||||||||||||||||||||||||||:|||||||||||| |||| | ||:|:|
Db        145 QSVLTQPPSVSAAPGQKVTISCSGSSSNIGNNYVSWYQQLPGTAPKLLIYGHTNRPAGVP 204

Qy         61 DRFSGSKSGTSATLGITGLQTGDEADYYCXTWDSSLSAVVFGGGTKLTVLG 111
              ||||||||||||:| |:| :: ||||||| || |||  ||||||||||||
Db        205 DRFSGSKSGTSASLAISGFRSEDEADYYCAAWDDSLSGWVFGGGTKLTVLG 255


RESULT 15
US-09-069-821-4
; Sequence 4, Application US/09069821
; Patent No. 6323322
;  GENERAL INFORMATION:
;    APPLICANT:  FILPULA, DAVID
;    APPLICANT:  WANG, MAOLIANG
;    APPLICANT:  SHORR, ROBERT
;    APPLICANT:  WHITLOW, MARC
;    APPLICANT:  LEE, LIHSYNG S.
;    TITLE OF INVENTION:  SINGLE-CHAIN ANTIGEN-BINDING PROTEINS
;    TITLE OF INVENTION:  CAPABLE OF GLYCOSYLATION, PRODUCTION AND USES THEREOF
;    NUMBER OF SEQUENCES:  33
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
;      STREET:  1100 NEW YORK AVE., NW, SUITE 600
;      CITY:  WASHINGTON
;      STATE:  DC
;      COUNTRY:  USA
;      ZIP:  20005
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/069,821
;      FILING DATE:  30-APR-1998
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/067,341
;      FILING DATE:  02-DEC-1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/063,074
;      FILING DATE:  27-OCT-1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/050,472
;      FILING DATE:  23-JUN-1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/044,449
;      FILING DATE:  30-APR-1997
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  KIM, JUDITH U.
;      REGISTRATION NUMBER:  40,679
;      REFERENCE/DOCKET NUMBER:  0977.2280003
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202)371-2600
;      TELEFAX:  (202)371-2540
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  262 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  not relevant
;    MOLECULE TYPE:  peptide
US-09-069-821-4

  Query Match             82.9%;  Score 486;  DB 3;  Length 262;
  Best Local Similarity   82.9%;  Pred. No. 2.5e-40;
  Matches   92;  Conservative    7;  Mismatches   12;  Indels    0;  Gaps    0;

Qy          1 QSVLTQPPSVSAAPGQKVTISCSGSSSNIGNNFVSWYQQLPGTAPXLLIYDITKRPSGIP 60
              ||||||||||||||||||||||||||||||:|||||||||||| |||| | ||:|:|
Db          1 QSVLTQPPSVSAAPGQKVTISCSGSSSNIGNNYVSWYQQLPGTAPKLLIYGHTNRPAGVP 60

Qy         61 DRFSGSKSGTSATLGITGLQTGDEADYYCXTWDSSLSAVVFGGGTKLTVLG 111
              ||||||||||||:| |:| :: ||||||| || |||  ||||||||||||
Db         61 DRFSGSKSGTSASLAISGFRSEDEADYYCAAWDDSLSGWVFGGGTKLTVLG 111


Search completed: October 13, 2005, 02:45:19
Job time : 18.5923 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: October 13, 2005, 02:45:26 ; Search time 113.511 Seconds
(without alignments)
514.286 Million cell updates/sec

Title: US-10-010-729A-9
Perfect score: 586
Sequence: 1 QSVLTQPPSVSAAPGQKVTI.....SLSAVVFGGGTKLTVLGQPK 114

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	524	89.4	111	1	LV1D_HUMAN	P01702 homo sapien
2	523	89.2	130	1	LV1G_HUMAN	P06316 homo sapien
3	515	87.9	110	2	Q8TE63	Q8te63 homo sapien
4	508	86.7	111	1	LV1C_HUMAN	P01701 homo sapien
5	507	86.5	235	2	Q6IN99	Q6in99 homo sapien
6	481	82.1	101	2	Q8IZD8	Q8izd8 homo sapien
7	472.5	80.6	236	2	Q6GMX4	Q6gmx4 homo sapien
8	468	79.9	109	1	LV1I_HUMAN	P06888 homo sapien
9	463	79.0	235	2	Q6GMW6	Q6gmw6 homo sapien
10	461.5	78.8	236	2	Q8NEJ1	Q8nej1 homo sapien
11	436.5	74.5	112	1	LV1B_HUMAN	P01700 homo sapien
12	436.5	74.5	236	2	Q6GMX3	Q6gmx3 homo sapien
13	430.5	73.5	236	2	Q96E61	Q96e61 homo sapien
14	430.5	73.5	236	2	Q6GMV7	Q6gmv7 homo sapien
15	421	71.8	237	2	Q6DHW4	Q6dhw4 homo sapien
16	420.5	71.8	236	2	Q6IPQ0	Q6ipq0 homo sapien
17	417.5	71.2	233	2	Q6PJA3	Q6pja3 homo sapien
18	417	71.2	109	1	LV1F_HUMAN	P04208 homo sapien
19	415.5	70.9	112	1	LV1H_HUMAN	P06887 homo sapien
20	415	70.8	111	1	LV1A_HUMAN	P01699 homo sapien
21	413.5	70.6	236	2	Q6PIQ7	Q6piq7 homo sapien
22	403	68.8	235	2	Q6PIK1	Q6pik1 homo sapien
23	400	68.3	108	2	Q96SB0	Q96sb0 homo sapien
24	394.5	67.3	236	2	Q6P5S3	Q6p5s3 homo sapien
25	386	65.9	116	2	Q96JD0	Q96jd0 homo sapien
26	385.5	65.8	234	2	Q8N355	Q8n355 homo sapien
27	385	65.7	111	1	LV2I_HUMAN	P01712 homo sapien
28	383.5	65.4	112	1	LV2K_HUMAN	P04209 homo sapien
29	382	65.2	111	1	LV2D_HUMAN	P01707 homo sapien
30	378.5	64.6	234	2	Q6GMW3	Q6gmw3 homo sapien
31	378	64.5	235	2	Q6PJG0	Q6pjg0 homo sapien
32	371	63.3	111	1	LV3B_HUMAN	P80748 homo sapien
33	369	63.0	111	1	LV2C_HUMAN	P01706 homo sapien
34	369	63.0	111	1	LV2G_HUMAN	P01710 homo sapien
35	368	62.8	111	1	LV2F_HUMAN	P01709 homo sapien
36	366	62.5	103	1	LV1E_HUMAN	P01703 homo sapien
37	364	62.1	111	1	LV2H_HUMAN	P01711 homo sapien
38	363	61.9	109	1	LV2E_HUMAN	P01708 homo sapien
39	363	61.9	235	2	Q6P2J1	Q6p2j1 homo sapien
40	362	61.8	233	2	Q6NS96	Q6ns96 homo sapien
41	360	61.4	106	1	LV4A_HUMAN	P01715 homo sapien
42	359	61.3	106	1	LV4E_HUMAN	P06889 homo sapien
43	359	61.3	111	1	LV2B_HUMAN	P01705 homo sapien
44	356	60.8	233	2	Q8TBC9	Q8tbc9 homo sapien
45	353	60.2	233	2	Q8N5F4	Q8n5f4 homo sapien

ALIGNMENTS

RESULT 1
LV1D_HUMAN
ID LV1D_HUMAN STANDARD; PRT; 111 AA.
AC P01702;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig lambda chain V-I region NIG-64.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=83186114; PubMed=6404900;
RA Kametani F., Takayasu T., Suzuki S., Shinoda T., Okuyama T.,
RA Shimizu A.;
RT "Comparative studies on the structure of the light chains of human
RT immunoglobulins. IV. Assignment of a subsubgroup.";
RL J. Biochem. 93:421-429(1983).
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A01965; L1HUNG.
DR HSSP; P01703; 7FAB.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Direct protein sequencing; Immunoglobulin V region;
KW Pyrrolidone carboxylic acid.
FT DOMAIN 1 105 Ig-like.
FT MOD_RES 1 1 Pyrrolidone carboxylic acid.
FT DISULFID 22 89 By similarity.
FT NON_TER 111 111
SQ SEQUENCE 111 AA; 11454 MW; A21C6121C18A61E0 CRC64;

Query Match 89.4%; Score 524; DB 1; Length 111;
Best Local Similarity 90.1%; Pred. No. 1.4e-43;
Matches 100; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

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Qy          1 QSVLTQPPSVSAAPGQKVTISCSGSSSNIGNNFVSWYQQLPGTAPXLLIYDITKRPSGIP 60
              ||||||||||||||||:|||||||||||||:||||||||||||| |||||  |||||||
Db          1 QSVLTQPPSVSAAPGQEVTISCSGSSSNIGDNFVSWYQQLPGTAPKLLIYDNNKRPSGIP 60

Qy         61 DRFSGSKSGTSATLGITGLQTGDEADYYCXTWDSSLSAVVFGGGTKLTVLG 111
              ||||||||||||||||||||||||||||| |||||||  :||||::||||
Db         61 DRFSGSKSGTSATLGITGLQTGDEADYYCGTWDSSLSVGMFGGGTRVTVLG 111
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RESULT 2
LV1G_HUMAN

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ID   LV1G_HUMAN     STANDARD;      PRT;   130 AA.
AC   P06316;
DT   01-JAN-1988 (Rel. 06, Created)
DT   01-JAN-1988 (Rel. 06, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig lambda chain V-I region BL2 precursor.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=85062823; PubMed=6095199;
RA   Tsujimoto Y., Croce C.M.;
RT   "Molecular cloning of a human immunoglobulin lambda chain variable
RT   sequence.";
RL   Nucleic Acids Res. 12:8407-8414(1984).
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; X01147; CAA25598.1; -.
DR   PIR; A01966; L1HUBL.
DR   HSSP; P01703; 7FAB.
DR   GO; GO:0005576; C:extracellular; NAS.
DR   GO; GO:0003823; F:antigen binding; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin V region; Signal.
FT   SIGNAL        1     19
FT   CHAIN        20    130       Ig lambda chain V-I region BL2.
FT   DOMAIN       20    115       V segment.
FT   DOMAIN      116    130       J segment.
FT   DISULFID     41    108       By similarity.
FT   NON_TER     130    130
SQ   SEQUENCE   130 AA;  13564 MW;  FA44BB17D3A55EBF CRC64;

  Query Match             89.2%;  Score 523;  DB 1;  Length 130;
  Best Local Similarity   90.1%;  Pred. No. 2e-43;
  Matches  100;  Conservative    5;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 QSVLTQPPSVSAAPGQKVTISCSGSSSNIGNNFVSWYQQLPGTAPXLLIYDITKRPSGIP 60
              ||||||||||||||||||||||||||||||::||||||:||||| |||||  |||||||
Db         20 QSVLTQPPSVSAAPGQKVTISCSGSSSNIGNDYVSWYQQVPGTAPKLLIYDNNKRPSGIP 79

Qy         61 DRFSGSKSGTSATLGITGLQTGDEADYYCXTWDSSLSAVVFGGGTKLTVLG 111
              ||||||||||||||||||||||||||||| ||::|||  ||||||||||||
Db         80 DRFSGSKSGTSATLGITGLQTGDEADYYCGTWNNSLSGWVFGGGTKLTVLG 130


RESULT 3
Q8TE63
ID   Q8TE63       PRELIMINARY;      PRT;   110 AA.
AC   Q8TE63;
DT   01-JUN-2002 (TrEMBLrel. 21, Created)
DT   01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Immunglobulin light chain variable region (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=95007525; PubMed=7923137;
RA   Hall B.L., Murray J.H., Haspel M.V., Kobrin B.J.;
RT   "Establishment, molecular rescue, and expression of 123AV16-1, a
RT   tumor-reactive human monoclonal antibody.";
RL   Cancer Res. 54:5178-5185(1994).
DR   EMBL; L33985; AAL68704.1; -.
DR   HSSP; P01703; 7FAB.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
FT   NON_TER       1      1
FT   CHAIN        <1    >110       immunoglobulin light chain variable
FT                                  region.
FT   NON_TER     110    110
SQ   SEQUENCE   110 AA;  11479 MW;  599D1628F8F5437C CRC64;

  Query Match             87.9%;  Score 515;  DB 2;  Length 110;
  Best Local Similarity   89.1%;  Pred. No. 1e-42;
  Matches   98;  Conservative    3;  Mismatches    9;  Indels    0;  Gaps    0;

Qy          1 QSVLTQPPSVSAAPGQKVTISCSGSSSNIGNNFVSWYQQLPGTAPXLLIYDITKRPSGIP 60
              || |||||||||||||||||||:|||||||||||||| |||||  |||||  |||||:|
Db          1 QSALTQPPSVSAAPGQKVTISCSGTSSNIGNNFVSWYQQFPGTAPKLLIYDNNKRPSGVP 60

Qy         61 DRFSGSKSGTSATLGITGLQTGDEADYYCXTWDSSLSAVVFGGGTKLTVL 110
              |||||||||||||||||||||||||||| ||| | | ||||||||||||
Db         61 DRFSGSKSGTSATLGITGLQTGDEADYYCGTWDTRLRAGVFGGGTKLTVL 110


RESULT 4
LV1C_HUMAN
ID   LV1C_HUMAN     STANDARD;      PRT;   111 AA.
AC   P01701;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Ig lambda chain V-I region NEW.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=69060892; PubMed=4177823;
RA   Langer B., Steinmetz-Kayne M., Hilschmann N.;
RT   "The complete amino acid sequence of Bence Jones protein New (lambda-
RT   type). Subgroups in the variable part of immunoglobulin L-chains of
RT   the lambda-type.";
RL   Hoppe-Seyler's Z. Physiol. Chem. 349:945-951(1968).
CC   -!- MISCELLANEOUS: This is a Bence-Jones protein.
CC   -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR   PIR; A01964; L1HUNW.
DR   HSSP; P01703; 7FAB.
DR   GO; GO:0005576; C:extracellular; NAS.
DR   GO; GO:0003823; F:antigen binding; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Bence-Jones protein; Direct protein sequencing;
KW   Immunoglobulin V region; Pyrrolidone carboxylic acid.
FT   DOMAIN        1    105       Ig-like.
FT   MOD_RES       1      1       Pyrrolidone carboxylic acid.
FT   DISULFID     22     89       By similarity.
FT   NON_TER     111    111
SQ   SEQUENCE   111 AA;  11453 MW;  AAECBCA3C49F2AD3 CRC64;

  Query Match             86.7%;  Score 508;  DB 1;  Length 111;
  Best Local Similarity   86.5%;  Pred. No. 5e-42;
  Matches   96;  Conservative    7;  Mismatches    8;  Indels    0;  Gaps    0;
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Qy          1 QSVLTQPPSVSAAPGQKVTISCSGSSSNIGNNFVSWYQQLPGTAPXLLIYDITKRPSGIP 60
              ||||||||||||||||||||||| |:|||||:|||:| |||||| ||||:  |||||||
Db          1 QSVLTQPPSVSAAPGQKVTISCSGGSTNIGNNYVSWHQHLPGTAPKLLIYEDNKRPSGIP 60

Qy         61 DRFSGSKSGTSATLGITGLQTGDEADYYCXTWDSSLSAVVFGGGTKLTVLG 111
              || | |||||||||||||:||||||||| ||||||:||||||||:||||
Db         61 DRISASKSGTSATLGITGLRTGDEADYYCATWDSSLNAVVFGGGTKVTVLG 111


RESULT 5
Q6IN99
ID   Q6IN99      PRELIMINARY;      PRT;   235 AA.
AC   Q6IN99;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   IGLC2 protein.
GN   Name=IGLC2;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Pancreas;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Pancreas;
RA   Strausberg R.;
RL   Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC072392; AAH72392.1; -.
DR   HSSP; P01842; 1AQK.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 1.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_1.
SQ   SEQUENCE   235 AA;  24888 MW;  90C95D5E87A6BCC1 CRC64;

  Query Match             86.5%;  Score 507;  DB 2;  Length 235;
  Best Local Similarity   85.1%;  Pred. No. 1.5e-41;
  Matches   97;  Conservative    6;  Mismatches   11;  Indels    0;  Gaps    0;

Qy          1 QSVLTQPPSVSAAPGQKVTISCSGSSSNIGNNFVSWYQQLPGTAPXLLIYDITKRPSGIP 60
              |||||||||||||||:||||||| ||||||::|||||| || || |||||  |||||||
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Db         20 QSVLTQPPSVSAAPGQRVTISCSGRSSNIGNSYVSWYQQFPGAAPQLLIYDNDKRPSGIP 79

Qy         61 DRFSGSKSGTSATLGITGLQTGDEADYYCXTWDSSLSAVVFGGGTKLTVLGQPK 114
              ||||||||||||| |||||| |||:||| |||:||:| |||||||||| |||
Db         80 DRFSGSKSGTSATLAITGLQTEDEAEYYCGTWDTSLTAGVFGGGTKLTVLSQPK 133


RESULT 6
Q8IZD8
ID   Q8IZD8      PRELIMINARY;      PRT;   101 AA.
AC   Q8IZD8;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Anti-thyroglobulin light chain variable region (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Jang Y.-J., Chung J., Park J.-Y.;
RL   Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY145444; AAN64328.1; -.
DR   HSSP; P01703; 7FAB.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
FT   NON_TER       1      1
FT   NON_TER     101    101
SQ   SEQUENCE   101 AA;  10374 MW;  1506C2D9AACBA793 CRC64;

  Query Match             82.1%;  Score 481;  DB 2;  Length 101;
  Best Local Similarity   90.1%;  Pred. No. 2e-39;
  Matches   91;  Conservative    5;  Mismatches    5;  Indels    0;  Gaps    0;

Qy         11 SAAPGQKVTISCSGSSSNIGNNFVSWYQQLPGTAPXLLIYDITKRPSGIPDRFSGSKSGT 70
              |||||||||||||||||||| |:|||||:||||| |||:|  |||||||||||||:|||
Db          1 SAAPGQKVTISCSGSSSNIGKNYVSWYQQVPGTAPQLLIHDTDKRPSGIPDRFSGSQSGT 60

Qy         71 SATLGITGLQTGDEADYYCXTWDSSLSAVVFGGGTKLTVLG 111
              |||||||||||||||||| |||:||||||||||||||||||
Db         61 SATLGITGLQTGDEADYYCGTWDTSLSAVVFGGGTKLTVLG 101


RESULT 7
Q6GMX4
ID   Q6GMX4      PRELIMINARY;      PRT;   236 AA.
AC   Q6GMX4;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Spleen;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
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RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Spleen;
RA   Strausberg R.;
RL   Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC073769; AAH73769.1; -.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 1.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW   Hypothetical protein.
SQ   SEQUENCE   236 AA;  24809 MW;  BA0AF0F4192364A5 CRC64;

  Query Match             80.6%;  Score 472.5;  DB 2;  Length 236;
  Best Local Similarity   80.0%;  Pred. No. 3.5e-38;
  Matches   92;  Conservative    9;  Mismatches   13;  Indels    1;  Gaps    1;

Qy          1 QSVLTQPPSVSAAPGQKVTISCSGSSSNIGNNF-VSWYQQLPGTAPXLLIYDITKRPSGI 59
              |||||||||||  ||||:|||||:|||||||  : | ||||||||||  ||||  : ||||:
Db         20 QSVLTQPPSVSGAPGQRVTISCTGSSSNIGAGYDVHWYQQLPGTAPRLLIYGNSNRPSGV 79

Qy         60 PDRFSGSKSGTSATLGITGLQTGDEADYYCXTWDSSLSAVVFGGGTKLTVLGQPK 114
              |||||||||||||:| |||||  |||||||  ::||||| |:|||||||||||||
Db         80 PDRFSGSKSGTSASLAITGLQAEDEADYYCQSYDSSLSGVMFGGGTKLTVLGQPK 134


RESULT 8
LV1I_HUMAN
ID   LV1I_HUMAN     STANDARD;      PRT;   109 AA.
AC   P06888;
DT   01-JAN-1988 (Rel. 06, Created)
DT   01-JAN-1988 (Rel. 06, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Ig lambda chain V-I region EPS.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=86000126; PubMed=3929803;
RA   Toft K.G., Sletten K., Husby G.;
RT   "The amino-acid sequence of the variable region of a carbohydrate-
RT   containing amyloid fibril protein EPS (immunoglobulin light chain,
RT   type lambda).";
RL   Biol. Chem. Hoppe-Seyler 366:617-625(1985).
CC   -!- MISCELLANEOUS: Residues 1-2, 56-62, and 74-78 and the sequenced
CC       peptides were positioned by homology.
CC   -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR   PIR; A24656; L1HUEP.
DR   HSSP; P01703; 7FAB.
DR   GO; GO:0005576; C:extracellular; NAS.
DR   GO; GO:0003823; F:antigen binding; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Amyloid; Direct protein sequencing; Glycoprotein;
KW   Immunoglobulin V region.
FT   DOMAIN        1    105       Ig-like.
FT   CARBOHYD    104    104       N-linked (GlcNAc. . .).
FT   DISULFID     22     89       By similarity.
FT   NON_TER     109    109
SQ   SEQUENCE   109 AA;  11414 MW;  556A313E24D5AC73 CRC64;

  Query Match             79.9%;  Score 468;  DB 1;  Length 109;
  Best Local Similarity   81.1%;  Pred. No. 4.1e-38;
  Matches   90;  Conservative    9;  Mismatches   10;  Indels    2;  Gaps    1;

Qy          1 QSVLTQPPSVSAAPGQKVTISCSGSSSNIGNNFVSWYQQLPGTAPXLLIYDITKRPSGIP 60
              |||||||||:||||||:|:|||||||||| |:| |||||||||| |||::  |||||||
Db          1 QSVLTQPPSLSAAPGQRVSISCSGSSSNIGKNYVDWYQQLPGTAPKLLIFNNNKRPSGIP 60

Qy         61 DRFSGSKSGTSATLGITGLQTGDEADYYCXTWDSSLSAVVFGGGTKLTVLG 111
              |||||||||||||||||||||||||| ||| |||:  |  |||||| :||:|
Db         61 DRFSGSKSGTSATLGITGLQTGDEAIYYCGTWDNRRS--VFGGGTNVTVVG 109


RESULT 9
Q6GMW6
ID   Q6GMW6      PRELIMINARY;      PRT;   235 AA.
AC   Q6GMW6;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Primary B-Cells;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Primary B-Cells;
RA   Strausberg R.;
RL   Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC073784; AAH73784.1; -.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 1.
DR   Pfam; PF00047; ig; 2.
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DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW   Hypothetical protein.
SQ   SEQUENCE   235 AA;  24803 MW;  058B05F61118F1B8 CRC64;

  Query Match             79.0%;  Score 463;  DB 2;  Length 235;
  Best Local Similarity   76.3%;  Pred. No. 3e-37;
  Matches   87;  Conservative   11;  Mismatches   16;  Indels    0;  Gaps    0;

Qy          1 QSVLTQPPSVSAAPGQKVTISCSGSSSNIGNNFVSWYQQLPGTAPXLLIYDITKRPSGIP 60
              |||||||||  |  ||:|||||||||||||||:| |:|||| ||||| ||||   :||||:|
Db         20 QSVLTQPPSASGTPGRRVTISCSGSSSNIGSNSVNWYQQFPGTAPRLLIYGNHQRPSGVP 79

Qy         61 DRFSGSKSGTSATLGITGLQTGDEADYYCXTWDSSLSAVVFGGGTKLTVLGQPK 114
              |||||||||||:| |:|||: ||||||| ||| ||:  ||| |||:|||||||
Db         80 DRFSGSKSGTSASLAISGLQSEDEADYYCGTWDDSLTGPVFGTGTKVTVLGQPK 133


RESULT 10
Q8NEJ1
ID   Q8NEJ1      PRELIMINARY;      PRT;   236 AA.
AC   Q8NEJ1;
DT   01-OCT-2002 (TrEMBLrel. 22, Created)
DT   01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Lung;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Lung;
RA   Strausberg R.;
RL   Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC030984; AAH30984.1; -.
DR   HSSP; P01703; 7FAB.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW   Hypothetical protein.
SQ   SEQUENCE   236 AA;  25024 MW;  1703B77942630E08 CRC64;

  Query Match             78.8%;  Score 461.5;  DB 2;  Length 236;
  Best Local Similarity   76.5%;  Pred. No. 4.2e-37;
  Matches   88;  Conservative   11;  Mismatches   15;  Indels    1;  Gaps    1;

Qy          1 QSVLTQPPSVSAAPGQKVTISCSGSSSNIGNNFVSWYQQLPGTAPXLLIYDITKRPSGIP 60
              |||||||||  |  :|||:|||||||| ||||:|:| ||||:|||||  ||||   :||||:|
Db         20 QSVLTQPPSASGSPGQRVTISCSGSRSNIGSNYVYWYQQVPGTAPKLLIYRNDQRPSGVP 79

Qy         61 DRFSGSKSGTSATLGITGLQTGDEADYYCXTWDSSLSA-VVFGGGTKLTVLGQPK 114
              |||||||||||:| |:||:: ||||||  || |||  |||||||||||| |||
Db         80 DRFSGSKSGTSASLAISGLRSEDEADYYCAAWDDSLSVHVVFGGGTKLTVLSQPK 134


RESULT 11
LV1B_HUMAN
ID   LV1B_HUMAN     STANDARD;      PRT;   112 AA.
AC   P01700;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Ig lambda chain V-I region HA.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=71103824; PubMed=5532227;
RA   Shinoda T., Titani K., Putnam F.W.;
RT   "Amino acid sequence of human lambda chains. II. Chymotryptic peptides
RT   and sequence of protein Ha.";
RL   J. Biol. Chem. 245:4475-4487(1970).
CC   -!- MISCELLANEOUS: This is a Bence-Jones protein.
CC   -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR   PIR; A01963; L1HUHA.
DR   HSSP; P01703; 7FAB.
DR   GO; GO:0005576; C:extracellular; NAS.
DR   GO; GO:0003823; F:antigen binding; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Bence-Jones protein; Direct protein sequencing;
KW   Immunoglobulin V region; Pyrrolidone carboxylic acid.
FT   DOMAIN        1    106       Ig-like.
FT   MOD_RES       1      1       Pyrrolidone carboxylic acid.
FT   DISULFID     22     90       By similarity.
FT   NON_TER     112    112
SQ   SEQUENCE   112 AA;  11896 MW;  8D73378F3F5CD039 CRC64;

  Query Match             74.5%;  Score 436.5;  DB 1;  Length 112;
  Best Local Similarity   76.6%;  Pred. No. 5.1e-35;
  Matches   85;  Conservative    9;  Mismatches   16;  Indels    1;  Gaps    1;

Qy          1 QSVLTQPPSVSAAPGQKVTISCSGSSSN-IGNNFVSWYQQLPGTAPXLLIYDITKRPSGI 59
              ||||||||||  |||:||||||| |||  |||:| |||||||||| ||||   |||||:
Db          1 QSVLTQPPSVSGTPGQRVTISCSGGSSNGTGNNYVYWYQQLPGTAPKLLIYRDDKRPSGV 60

Qy         60 PDRFSGSKSGTSATLGITGLQTGDEADYYCXTWDSSLSAVVFGGGTKLTVL 110
              |||||||||||||:| |:||:: ||| |:|  ||  ||||||||||:||||
Db         61 PDRFSGSKSGTSASLAISGLRSEDEAHYHCAAWDYRLSAVVFGGGTQLTVL 111


RESULT 12
Q6GMX3
ID   Q6GMX3      PRELIMINARY;      PRT;   236 AA.
AC   Q6GMX3;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
```

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DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Spleen;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Spleen;
RA   Strausberg R.;
RL   Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC073770; AAH73770.1; -.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 1.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW   Hypothetical protein.
SQ   SEQUENCE   236 AA;  24700 MW;  BC0BB94DF4F2DCB7 CRC64;

  Query Match             74.5%;  Score 436.5;  DB 2;  Length 236;
  Best Local Similarity   74.8%;  Pred. No. 1.2e-34;
  Matches   86;  Conservative   10;  Mismatches   18;  Indels    1;  Gaps    1;

Qy          1 QSVLTQPPSVSAAPGQKVTISCSGSSSNIGNNF-VSWYQQLPGTAPXLLIYDITKRPSGI 59
              |||||||||||| |||| |||||:|||||||  : | ||||||||||| ||| : : ||||:
Db         20 QSVLTQPPSVSGAPGQGVTISCTGSSSNIGAGYGVHWYQQLPGTAPKLLISNNSNRPSGV 79

Qy         60 PDRFSGSKSGTSATLGITGLQTGDEADYYCXTWDSSLSAVVFGGGTKLTVLGQPK 114
              |||||||||||||:| | |||  ||||||| ::| ||:  ||||||:|||| |||
Db         80 PDRFSGSKSGTSASLAIAGLQAEDEADYYCQSYDDSLTGRVFGGGTRLTVLSQPK 134


RESULT 13
Q96E61
ID   Q96E61      PRELIMINARY;      PRT;   236 AA.
AC   Q96E61;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RA   Strausberg R.;
RL   Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC012876; AAH12876.1; -.
DR   PIR; S12440; S12440.
DR   HSSP; P01842; 1AQK.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW   Hypothetical protein.
SQ   SEQUENCE   236 AA;  24712 MW;  7EC9FB3622FED957 CRC64;

  Query Match             73.5%;  Score 430.5;  DB 2;  Length 236;
  Best Local Similarity   73.0%;  Pred. No. 4.5e-34;
  Matches   84;  Conservative    9;  Mismatches   21;  Indels    1;  Gaps    1;

Qy          1 QSVLTQPPSVSAAPGQKVTISCSGSSSNIGNNF-VSWYQQLPGTAPXLLIYDITKRPSGI 59
              |||| |||||| |||| |||||:|||:|||  : | |||| || || :|||    ||||:
Db         20 QSVLAQPPSVSGAPGQTVTISCTGSSTNIGAGYAVHWYQQFPGAAPKVLIYGNYNRPSGV 79

Qy         60 PDRFSGSKSGTSATLGITGLQTGDEADYYCXTWDSSLSAVVFGGGTKLTVLGQPK 114
              |||||||||||||:| |||||  ||||||| ::| |||  ||| |||:|||||||
Db         80 PDRFSGSKSGTSASLAITGLQAEDEADYYCQSYDGSLSGSVFGAGTKVTVLGQPK 134


RESULT 14
Q6GMV7
ID   Q6GMV7      PRELIMINARY;      PRT;   236 AA.
AC   Q6GMV7;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
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```
RC   TISSUE=Spleen;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Spleen;
RA   Strausberg R.;
RL   Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC073795; AAH73795.1; -.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 1.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW   Hypothetical protein.
SQ   SEQUENCE   236 AA;  24950 MW;  3B0477247847E930 CRC64;

  Query Match             73.5%;  Score 430.5;  DB 2;  Length 236;
  Best Local Similarity   73.0%;  Pred. No. 4.5e-34;
  Matches   84;  Conservative   11;  Mismatches   19;  Indels    1;  Gaps    1;

Qy          1 QSVLTQPPSVSAAPGQKVTISCSGSSSNIGNNFVSWYQQLPGTAPXLLIYDITKRPSGIP 60
              |||||||  |||  |||:|||||||||||||| | |:|||||||||| |||:   :||||:|
Db         20 QSVLTQPSSVSGTPGQRVTISCSGSSSNIGANNVNWYQQLPGTAPKLLIHTTNQRPSGVP 79

Qy         61 DRFSGSKSGTSATLGITGLQTGDEADYYCXTWDSSLSA-VVFGGGTKLTVLGQPK 114
              :|||||||| ||:| |:|||: |||:|||  || ||    ||| |||:|||||||
Db         80 ERFSGSKSGPSASLVISGLQSEDEAEYYCAAWDDSLDGPYVFGTGTKVTVLGQPK 134


RESULT 15
Q6DHW4
ID   Q6DHW4      PRELIMINARY;      PRT;   237 AA.
AC   Q6DHW4;
DT   25-OCT-2004 (TrEMBLrel. 28, Created)
DT   25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT   25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Primary B-Cells;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Primary B-Cells;
RA   Strausberg R.;
RL   Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC075843; AAH75843.1; -.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 1.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW   Hypothetical protein.
SQ   SEQUENCE   237 AA;  25108 MW;  6814170F7E784825 CRC64;

  Query Match             71.8%;  Score 421;  DB 2;  Length 237;
  Best Local Similarity   70.7%;  Pred. No. 3.9e-33;
  Matches   82;  Conservative   11;  Mismatches   21;  Indels    2;  Gaps    1;

Qy          1 QSVLTQPPSVSAAPGQKVTISCSGSSSNIGNNFVSWYQQLPGTAPXLLIYDITKRPSGIP 60
              ||:||||||||  |||:|||||||||||||| |:| ||||:|||||  |||    :||||:|
Db         20 QSLLTQPPSVSGTPGQRVTISCSGSSSNIGINYVYWYQQIPGTAPKLLISTNDQRPSGVP 79

Qy         61 DRFSGSKSGTSATLGITGLQTGDEADYYCXTWDSSLS--AVVFGGGTKLTVLGQPK 114
              |||||||||||:| | ||:: ||| |||  || |:|     || |||:||| |||
Db         80 DRFSGSKSGTSASLAIGGLRSEDEAHYYCAAWDDSMSGPGYAFGTGTKVTVLRQPK 135


Search completed: October 13, 2005, 03:10:53
Job time : 114.511 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: October 13, 2005, 02:57:16 ; Search time 23.485 Seconds
(without alignments)
467.052 Million cell updates/sec

Title: US-10-010-729A-9
Perfect score: 586
Sequence: 1 QSVLTQPPSVSAAPGQKVTI.....SLSAVVFGGGTKLTVLGQPK 114

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	560	95.6	235	2	S05270	Ig lambda chain pr
2	539	92.0	111	2	S47009	Ig lambda chain V1
3	538	91.8	130	2	S09712	Ig lambda chain V
4	534	91.1	113	2	A29700	Ig lambda chain V
5	533	91.0	232	2	S25742	Ig lambda chain -
6	526	89.8	131	2	S24321	Ig lambda chain pr
7	524	89.4	111	1	L1HUNG	Ig lambda chain V-
8	523	89.2	130	1	L1HUBL	Ig lambda chain pr
9	520	88.7	111	2	S19664	Ig lambda chain V
10	508	86.7	111	1	L1HUNW	Ig lambda chain V-
11	486	82.9	111	2	S47185	Ig lambda chain -
12	485	82.8	98	2	S36050	Ig lambda chain -
13	485	82.8	233	2	S25752	Ig lambda chain -
14	477	81.4	130	2	S78057	Ig lambda chain pr
15	474	80.9	216	2	A42193	Ig lambda chain (B
16	468	79.9	109	1	L1HUEP	Ig lambda chain V-
17	467	79.7	234	2	S25757	Ig lambda chain -
18	462	78.8	129	2	S78058	Ig lambda chain pr
19	462	78.8	233	2	S25744	Ig lambda chain -
20	462	78.8	235	2	S25750	Ig lambda chain -
21	461.5	78.8	149	2	S23626	Ig lambda chain V
22	459	78.3	216	2	S29258	Ig lambda chain V
23	457.5	78.1	213	2	S21066	Ig lambda chain V
24	452	77.1	112	2	B44151	Ig lambda chain V
25	451	77.0	112	2	C44151	Ig lambda chain V
26	447.5	76.4	140	2	PH0134	Ig lambda chain pr
27	447.5	76.4	236	2	S25746	Ig lambda chain -
28	447	76.3	112	2	D44151	Ig lambda chain V
29	443	75.6	216	2	S03401	Ig lambda chain (K
30	442.5	75.5	235	2	S25754	Ig lambda chain -
31	440	75.1	110	2	S57408	Ig lambda chain V-
32	436.5	74.5	112	1	L1HUHA	Ig lambda chain V-
33	436	74.4	112	2	A44151	Ig lambda chain V
34	435.5	74.3	112	2	S51148	antibody light cha
35	434.5	74.1	217	2	JE0246	Ig lambda chain NI
36	432	73.7	110	2	S57428	Ig light chain V-J
37	429	73.2	111	2	S36274	Ig lambda chain V
38	420	71.7	145	2	S25743	Ig lambda chain -
39	419	71.5	98	2	S36068	Ig lambda chain -
40	419	71.5	117	2	S04525	Ig lambda chain pr
41	417	71.2	109	1	L1HUWA	Ig lambda chain V-
42	415.5	70.9	112	1	L1HUMM	Ig lambda chain V-
43	415.5	70.9	140	2	PH0132	Ig lambda chain pr
44	415	70.8	111	1	L1HUVO	Ig lambda chain V-
45	409	69.8	111	2	S36263	Ig lambda chain V

ALIGNMENTS

RESULT 1
S05270
Ig lambda chain precursor - human
C;Species: Homo sapiens (man)
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 21-Jan-2000
C;Accession: S05270; S04601
R;Kishimoto, T.
submitted to the EMBL Data Library, March 1989
A;Reference number: S05270
A;Accession: S05270
A;Molecule type: mRNA
A;Residues: 1-235 <KIS1>
A;Cross-references: EMBL:X14583; NID:g33394; PIDN:CAA32725.1; PID:g33395
R;Kishimoto, T.; Okajima, H.; Okumoto, T.; Taniguchi, M.
Nucleic Acids Res. 17, 4385, 1989
A;Title: Nucleotide sequences of the cDNAs encoding the V-regions of H- and L-chains of
A;Reference number: S04601; MUID:89296497; PMID:2500644
A;Accession: S04601
A;Molecule type: mRNA
A;Residues: 1-130 <KIS2>
A;Cross-references: EMBL:X14583
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-235/Product: Ig lambda chain #status predicted <MAT>
F;150-218/Domain: immunoglobulin homology <IMM>

Query Match 95.6%; Score 560; DB 2; Length 235;
Best Local Similarity 94.7%; Pred. No. 8.9e-41;
Matches 108; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

```
Qy          1 QSVLTQPPSVSAAPGQKVTISCSGSSSNIGNNFVSWYQQLPGTAPXLLIYDITKRPSGIP 60
              ||||||||||||||||||||||||||||||:||||||||||| |||||  |||||||
Db         20 QSVLTQPPSVSAAPGQKVTISCSGSSSNIGNNYVSWYQQLPGTAPKLLIYDNNKRPSGIP 79

Qy         61 DRFSGSKSGTSATLGITGLQTGDEADYYCXTWDSSLSAVVFGGGTKLTVLGQPK 114
              |||||||||||||||||||||||||||| |||||||| ||||||||||||||
Db         80 DRFSGSKSGTSATLGITGLQTGDEADYYCGTWDSSLSAGVFGGGTKLTVLGQPK 133
```

RESULT 2
S47009
Ig lambda chain V1-J3 region - human
C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 21-Jan-2000
C;Accession: S47009
R;Mahmoudi, M.; Gasyna, E.; Denomme, G.; Edwards, J.; Bell, D.; Cairns, E.
submitted to the EMBL Data Library, July 1994
A;Description: The role of the immunoglobulin heavy chain in human anti-DNA antibody bin
A;Reference number: S47009
A;Accession: S47009
A;Status: preliminary

```
A;Molecule type: mRNA
A;Residues: 1-111 <MAH>
A;Cross-references: EMBL:Z35495; NID:g517346; PIDN:CAA84629.1; PID:g517347
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-91/Domain: immunoglobulin homology <IMM>

  Query Match             92.0%;  Score 539;  DB 2;  Length 111;
  Best Local Similarity   93.7%;  Pred. No. 2.6e-39;
  Matches  104;  Conservative    2;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 QSVLTQPPSVSAAPGQKVTISCSGSSSNIGNNFVSWYQQLPGTAPXLLIYDITKRPSGIP 60
              ||||||||||||||||||||||||||||||||:||||||||||| ||||:  |||||||
Db          1 QSVLTQPPSVSAAPGQKVTISCSGSSSNIGNNYVSWYQQLPGTAPKLLIYENNKRPSGIP 60

Qy         61 DRFSGSKSGTSATLGITGLQTGDEADYYCXTWDSSLSAVVFGGGTKLTVLG 111
              ||||||||||||||||||||||||||||| |||||||| ||||||||||||
Db         61 DRFSGSKSGTSATLGITGLQTGDEADYYCGTWDSSLSAGVFGGGTKLTVLG 111


RESULT 3
S09712
Ig lambda chain V region - human
C;Species: Homo sapiens (man)
C;Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C;Accession: S09712
R;Hughes-Jones, N.C.; Bye, J.M.; Beale, D.; Coadwell, J.
Biochem. J. 268, 135-140, 1990
A;Title: Nucleotide sequences and three-dimensional modelling of the VH and VL domains c
A;Reference number: S09710; MUID:90262535; PMID:2111699
A;Accession: S09712
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-130 <HUG>
A;Cross-references: GB:X52109; NID:g31454; PIDN:CAA36343.1; PID:g31455
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;34-110/Domain: immunoglobulin homology <IMM>

  Query Match             91.8%;  Score 538;  DB 2;  Length 130;
  Best Local Similarity   93.6%;  Pred. No. 3.8e-39;
  Matches  103;  Conservative    3;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 QSVLTQPPSVSAAPGQKVTISCSGSSSNIGNNFVSWYQQLPGTAPXLLIYDITKRPSGIP 60
              |||||||||||||||||||||||:|||||||:|||||||||||| |||||  |||||||
Db         20 QSVLTQPPSVSAAPGQKVTISCSGTSSNIGNNYVSWYQQLPGTAPKLLIYDNNKRPSGIP 79

Qy         61 DRFSGSKSGTSATLGITGLQTGDEADYYCXTWDSSLSAVVFGGGTKLTVL 110
              ||||||||||||||||||:||||||||| ||||||||||||||||||||
Db         80 DRFSGSKSGTSATLGITGLRTGDEADYYCATWDSSLSAVVFGGGTKLTVL 129


RESULT 4
A29700
Ig lambda chain V region (Zim) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 21-Jan-2000
C;Accession: A29700
R;Eulitz, M.; Breuer, M.; Linke, R.P.
Biol. Chem. Hoppe-Seyler 368, 863-870, 1987
A;Title: Is the formation of AL-type amyloid promoted by structural peculiarities of imm
A;Reference number: A29700; MUID:87299022; PMID:3620114
A;Accession: A29700
A;Molecule type: protein
A;Residues: 1-113 <EUL>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;14-90/Domain: immunoglobulin homology <IMM>

  Query Match             91.1%;  Score 534;  DB 2;  Length 113;
  Best Local Similarity   90.3%;  Pred. No. 7.2e-39;
  Matches  102;  Conservative    3;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          2 SVLTQPPSVSAAPGQKVTISCSGSSSNIGNNFVSWYQQLPGTAPXLLIYDITKRPSGIPD 61
              |:|||||||||||||||||||||||||||||:|||||||||||| ||||:  ||||||||
Db          1 SLLTQPPSVSAAPGQKVTISCSGSSSNIGNNYVSWYQQLPGTAPRLLIYENDKRPSGIPD 60

Qy         62 RFSGSKSGTSATLGITGLQTGDEADYYCXTWDSSLSAVVFGGGTKLTVLGQPK 114
              ||||||| | |||||||||||||||| |||||||| ||||||||||||||||
Db         61 RFSGSKSDASVTLGITGLQTGDEADYYCGTWDSSLSAAVFGGGTKLTVLGQPK 113


RESULT 5
S25742
Ig lambda chain - human
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C;Accession: S25742
R;Combriato, G.; Klobeck, H.G.
Eur. J. Immunol. 21, 1513-1522, 1991
A;Title: V(lambda) and J(lambda)-C(lambda) gene segments of the human immunoglobulin lamb
A;Reference number: S16439; MUID:91257162; PMID:1904362
A;Accession: S25742
A;Status: preliminary; translation not shown
A;Molecule type: mRNA
A;Residues: 1-232 <COM>
A;Cross-references: EMBL:X57806; NID:g33709; PIDN:CAA40944.1; PID:g33710
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;147-215/Domain: immunoglobulin homology <IMM>

  Query Match             91.0%;  Score 533;  DB 2;  Length 232;
  Best Local Similarity   89.5%;  Pred. No. 1.8e-38;
  Matches  102;  Conservative    4;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          1 QSVLTQPPSVSAAPGQKVTISCSGSSSNIGNNFVSWYQQLPGTAPXLLIYDITKRPSGIP 60
              |||||||||||||||||||||||||||||:|||||||| || |||::  |||| ||
Db         17 QSVLTQPPSVSAAPGQKVTISCSGSSSNIGNNYVSWYQQLPGRAPKLLIFENNKRPSAIP 76

Qy         61 DRFSGSKSGTSATLGITGLQTGDEADYYCXTWDSSLSAVVFGGGTKLTVLGQPK 114
              |||||||||||||||| |||||||||||| ||||||: ||||||||||||||||
Db         77 DRFSGSKSGTSATLGIAGLQTGDEADYYCGTWDSSLTDVVFGGGTKLTVLGQPK 130


RESULT 6
S24321
Ig lambda chain precursor - human
C;Species: Homo sapiens (man)
C;Date: 02-Dec-1993 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C;Accession: S24321
R;Aucouturier, P.; Khamlichi, A.A.; Preud'homme, J.L.; Bauwens, M.; Touchard, G.; Cogne,
Biochem. J. 285, 149-152, 1992
A;Title: Complementary DNA sequence of human amyloidogenic immunoglobulin light-chain pr
A;Reference number: S24319; MUID:92344562; PMID:1379039
A;Accession: S24321
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-131 <AUC>
A;Cross-references: EMBL:X64134; NID:g32808; PIDN:CAA45495.1; PID:g32809
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;34-110/Domain: immunoglobulin homology <IMM>

  Query Match             89.8%;  Score 526;  DB 2;  Length 131;
  Best Local Similarity   90.2%;  Pred. No. 4e-38;
  Matches  101;  Conservative    3;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          1 QSVLTQPPSVSAAPGQKVTISCSGSSSNIGNNFVSWYQQLPGTAPXLLIYDITKRPSGIP 60
              |||||||||||||||||||||||||||||| ||:||||||||| || ||||:  |||||||
Db         20 QSVLTQPPSVSAAPGQKVTISCSGSSSNIANNYVSWYQQLPGAAPKLLIYENVKRPSGIP 79

Qy         61 DRFSGSKSGTSATLGITGLQTGDEADYYCXTWDSSLSAVVFGGGTKLTVLGQ 112
              ||||||||||||||||||||||||:||| ||||||| | ||||||||||||
Db         80 DRFSGSKSGTSATLGITGLQTGDEAEYYCGTWDSSLSGVEFGGGTKLTVLGQ 131
```

```
RESULT 7
L1HUNG
Ig lambda chain V-I region (Nig-64) - human (tentative sequence)
C;Species: Homo sapiens (man)
C;Date: 03-Aug-1984 #sequence_revision 03-Aug-1984 #text_change 09-Jul-2004
C;Accession: A01965
R;Kametani, F.; Takayasu, T.; Suzuki, S.; Shinoda, T.; Okuyama, T.; Shimizu, A.
J. Biochem. 93, 421-429, 1983
A;Title: Comparative studies on the structure of the light chains of human immunoglobuli
A;Reference number: A91970; MUID:83186114; PMID:6404900
A;Accession: A01965
A;Molecule type: protein
A;Residues: 1-111 <KAM>
A;Cross-references: UNIPROT:P01702
C;Genetics:
A;Gene: GDB:IGLV@
A;Cross-references: GDB:119342; OMIM:147240
A;Map position: 22q11.2-22q11.2
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: blocked amino end; heterotetramer
F;15-91/Domain: immunoglobulin homology <IMM>
F;1/Modified site: blocked amino end (Gln) (probably pyrrolidone carboxylic acid) #statu
F;22-89/Disulfide bonds: #status predicted

  Query Match             89.4%;  Score 524;  DB 1;  Length 111;
  Best Local Similarity   90.1%;  Pred. No. 5e-38;
  Matches  100;  Conservative    5;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 QSVLTQPPSVSAAPGQKVTISCSGSSSNIGNNFVSWYQQLPGTAPXLLIYDITKRPSGIP 60
              ||||||||||||||||:|||||||||||:|||||||||||||| |||||  |||||||
Db          1 QSVLTQPPSVSAAPGQEVTISCSGSSSNIGDNFVSWYQQLPGTAPKLLIYDNNKRPSGIP 60

Qy         61 DRFSGSKSGTSATLGITGLQTGDEADYYCXTWDSSLSAVVFGGGTKLTVLG 111
              |||||||||||||||||||||||||||| |||||||  :|||||::||||
Db         61 DRFSGSKSGTSATLGITGLQTGDEADYYCGTWDSSLSVGMFGGGTRVTVLG 111


RESULT 8
L1HUBL
Ig lambda chain precursor V-I region (BL2) - human
C;Species: Homo sapiens (man)
C;Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 09-Jul-2004
C;Accession: A01966
R;Tsujimoto, Y.; Croce, C.M.
Nucleic Acids Res. 12, 8407-8414, 1984
A;Title: Molecular cloning of a human immunoglobulin lambda chain variable sequence.
A;Reference number: A01966; MUID:85062823; PMID:6095199
A;Accession: A01966
A;Molecule type: mRNA
A;Residues: 1-130 <TSU>
A;Cross-references: UNIPROT:P06316; GB:X01147; NID:g33335; PIDN:CAA25598.1; PID:g758087
C;Genetics:
A;Gene: GDB:IGLV@
A;Cross-references: GDB:119342; OMIM:147240
A;Map position: 22q11.2-22q11.2
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-130/Product: Ig lambda chain V-I region (BL2) #status predicted <MAT>
F;20-115/Region: V segment
F;34-110/Domain: immunoglobulin homology <IMM>
F;116-130/Region: J segment
F;41-108/Disulfide bonds: #status predicted

  Query Match             89.2%;  Score 523;  DB 1;  Length 130;
  Best Local Similarity   90.1%;  Pred. No. 7.1e-38;
  Matches  100;  Conservative    5;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 QSVLTQPPSVSAAPGQKVTISCSGSSSNIGNNFVSWYQQLPGTAPXLLIYDITKRPSGIP 60
              ||||||||||||||||||||||||||||::||||||:||||| |||||  |||||||
Db         20 QSVLTQPPSVSAAPGQKVTISCSGSSSNIGNDYVSWYQQVPGTAPKLLIYDNNKRPSGIP 79

Qy         61 DRFSGSKSGTSATLGITGLQTGDEADYYCXTWDSSLSAVVFGGGTKLTVLG 111
              |||||||||||||||||||||||||||| ||::|||  ||||||||||||
Db         80 DRFSGSKSGTSATLGITGLQTGDEADYYCGTWNNSLSGWVFGGGTKLTVLG 130


RESULT 9
S19664
Ig lambda chain V region (clone alpha-phOx15) - human
C;Species: Homo sapiens (man)
C;Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 20-Jun-2000
C;Accession: S19664; S24444
R;Marks, J.D.; Hoogenboom, H.R.; Bonnert, T.P.; McCafferty, J.; Griffiths, A.D.; Winter,
J. Mol. Biol. 222, 581-597, 1991
A;Title: By-passing immunization. Human antibodies from V-gene libraries displayed on ph
A;Reference number: S19663; MUID:92085276; PMID:1748994
A;Accession: S19664
A;Molecule type: mRNA
A;Residues: 1-111 <MAR>
A;Cross-references: EMBL:X61641
R;Jones, P.T.
submitted to the EMBL Data Library, October 1991
A;Reference number: S24442
A;Accession: S24444
A;Molecule type: mRNA
A;Residues: 1-110,'W' <JON>
A;Cross-references: EMBL:X61641; NID:g35458; PIDN:CAA43822.1; PID:g1335271
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-91/Domain: immunoglobulin homology <IMM>

  Query Match             88.7%;  Score 520;  DB 2;  Length 111;
  Best Local Similarity   89.2%;  Pred. No. 1.1e-37;
  Matches   99;  Conservative    3;  Mismatches    9;  Indels    0;  Gaps    0;

Qy          1 QSVLTQPPSVSAAPGQKVTISCSGSSSNIGNNFVSWYQQLPGTAPXLLIYDITKRPSGIP 60
              ||||||||||||||||||||||||||||||:||||| |||||  |||||||
Db          1 QSVLTQPPSVSAAPGQKVTISCSGSSSNIGNNYVSWYQHLPGTAPNLLIYDNNKRPSGIP 60

Qy         61 DRFSGSKSGTSATLGITGLQTGDEADYYCXTWDSSLSAVVFGGGTKLTVLG 111
              |||||||||||||||||||||||||||| |||  |:| ||| |||:||||
Db         61 DRFSGSKSGTSATLGITGLQTGDEADYYCGTWDGRLTAAVFGSGTKVTVLG 111


RESULT 10
L1HUNW
Ig lambda chain V-I region (New) - human
C;Species: Homo sapiens (man)
C;Date: 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change 09-Jul-2004
C;Accession: A01964
R;Langer, B.; Steinmetz-Kayne, M.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 349, 945-951, 1968
A;Title: The complete amino acid sequence of Bence-Jones protein New (lambda type). Subg
A;Reference number: A01964; MUID:69060892; PMID:4177823
A;Accession: A01964
A;Molecule type: protein
A;Residues: 1-111 <LAN>
A;Cross-references: UNIPROT:P01701
C;Comment: This is a Bence Jones protein.
C;Genetics:
A;Gene: GDB:IGLV@
A;Cross-references: GDB:119342; OMIM:147240
A;Map position: 22q11.2-22q11.2
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: blocked amino end; heterotetramer
F;15-91/Domain: immunoglobulin homology <IMM>
F;1/Modified site: blocked amino end (Gln) (probably pyrrolidone carboxylic acid) #statu
F;22-89/Disulfide bonds: #status predicted
```

```
  Query Match             86.7%;  Score 508;  DB 1;  Length 111;
  Best Local Similarity   86.5%;  Pred. No. 1.2e-36;
  Matches   96;  Conservative    7;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          1 QSVLTQPPSVSAAPGQKVTISCSGSSSNIGNNFVSWYQQLPGTAPXLLIYDITKRPSGIP 60
              ||||||||||||||||||||||||| |:|||||:|||:| |||||| ||||:  |||||||
Db          1 QSVLTQPPSVSAAPGQKVTISCSGGSTNIGNNYVSWHQHLPGTAPKLLIYEDNKRPSGIP 60

Qy         61 DRFSGSKSGTSATLGITGLQTGDEADYYCXTWDSSLSAVVFGGGTKLTVLG 111
              || | |||||||||||||:||||||||| ||||||:|||||||||:||||
Db         61 DRISASKSGTSATLGITGLRTGDEADYYCATWDSSLNAVVFGGGTKVTVLG 111


RESULT 11
S47185
Ig lambda chain - human
C;Species: Homo sapiens (man)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000
C;Accession: S47185
R;McIntosh, R.S.; Tandon, N.; Metcalfe, R.A.; Weetman, A.P.
submitted to the EMBL Data Library, June 1994
A;Description: Cloning and analysis of IgM anti-thyroglobulin autoantibodies from patien
A;Reference number: S47181
A;Accession: S47185
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-111 <MCI>
A;Cross-references: EMBL:X79782; NID:g506428; PIDN:CAA56178.1; PID:g506429
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;14-90/Domain: immunoglobulin homology <IMM>

  Query Match             82.9%;  Score 486;  DB 2;  Length 111;
  Best Local Similarity   86.5%;  Pred. No. 8.7e-35;
  Matches   96;  Conservative    3;  Mismatches   10;  Indels    2;  Gaps    1;

Qy          2 SVLTQPPSVSAAPGQKVTISCSGSSSNIGNNFVSWYQQLPGTAPXLLIYDITKRPSGIPD 61
              | ||||||||||||:|||||||||||||| |:|||||||||||| ||||   ||||||||
Db          1 SELTQPPSVSAAPGQRVTISCSGSSSNIGKNYVSWYQQLPGTAPKLLIYKNNKRPSGIPD 60

Qy         62 RFSGSKSGTSATLGITGLQTGDEADYYCXTWDSSLSA--VVFGGGTKLTVL 110
              |||||||||||||||| |||||||||| |||||||    :||||||||||
Db         61 RFSGSKSGTSATLGITRLQTGDEADYYCGTWDSSLSGGRGIFGGGTKLTVL 111


RESULT 12
S36050
Ig lambda chain - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 01-Dec-1995 #text_change 21-Jan-2000
C;Accession: S36050
R;Williams, S.C.
submitted to the EMBL Data Library, April 1993
A;Reference number: S36046
A;Accession: S36050
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-98 <WIL>
A;Cross-references: EMBL:Z22191; NID:g312298; PIDN:CAA80201.1; PID:g312299
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-91/Domain: immunoglobulin homology <IMM>

  Query Match             82.8%;  Score 485;  DB 2;  Length 98;
  Best Local Similarity   94.9%;  Pred. No. 9.4e-35;
  Matches   93;  Conservative    1;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 QSVLTQPPSVSAAPGQKVTISCSGSSSNIGNNFVSWYQQLPGTAPXLLIYDITKRPSGIP 60
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Db          1 QSVLTQPPSVSAAPGQKVTISCSGSSSNIGNNYVSWYQQLPGTAPKLLIYDNNKRPSGIP 60

Qy         61 DRFSGSKSGTSATLGITGLQTGDEADYYCXTWDSSLSA 98
              |||||||||||||||||||||||||||||| ||||||||
Db         61 DRFSGSKSGTSATLGITGLQTGDEADYYCGTWDSSLSA 98


RESULT 13
S25752
Ig lambda chain - human
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C;Accession: S25752
R;Combriato, G.; Klobeck, H.G.
Eur. J. Immunol. 21, 1513-1522, 1991
A;Title: V(lambda) and J(lambda)-C(lambda) gene segments of the human immunoglobulin lam
A;Reference number: S16439; MUID:91257162; PMID:1904362
A;Accession: S25752
A;Status: preliminary; translation not shown
A;Molecule type: mRNA
A;Residues: 1-233 <COM>
A;Cross-references: EMBL:X57817; NID:g33733; PIDN:CAA40954.1; PID:g33734
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;148-216/Domain: immunoglobulin homology <IMM>

  Query Match             82.8%;  Score 485;  DB 2;  Length 233;
  Best Local Similarity   79.8%;  Pred. No. 2.2e-34;
  Matches   91;  Conservative    9;  Mismatches   14;  Indels    0;  Gaps    0;

Qy          1 QSVLTQPPSVSAAPGQKVTISCSGSSSNIGNNFVSWYQQLPGTAPXLLIYDITKRPSGIP 60
              ||||||||| |  |||:|||||||||||||:| |:|||||||||| ||||   :||||:|
Db         18 QSVLTQPPSASGTPGQRVTISCSGSSSNIGSNTVNWYQQLPGTAPKLLIYRNNQRPSGVP 77

Qy         61 DRFSGSKSGTSATLGITGLQTGDEADYYCXTWDSSLSAVVFGGGTKLTVLGQPK 114
              |||||||||||:| |:|||: |||||||  || ||: ||||||||||||||||
Db         78 DRFSGSKSGTSASLAISGLQSEDEADYYCAAWDDSLNGVVFGGGTKLTVLGQPK 131


RESULT 14
S78057
Ig lambda chain precursor V-J region (clone mAB 61VL) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 19-Nov-1997 #sequence_revision 05-Dec-1997 #text_change 23-Jul-1999
C;Accession: S78057; S23722
R;Harindranath, N.
submitted to the EMBL Data Library, August 1990
A;Reference number: S78051
A;Accession: S78057
A;Molecule type: mRNA
A;Residues: 1-130 <HAR>
A;Cross-references: EMBL:X54438; NID:g37920; PIDN:CAA38307.1; PID:g37921
R;Harindranath, N.; Goldfarb, I.S.; Ikematsu, H.; Burastero, S.E.; Wilder, R.L.; Notkins
Int. Immunol. 3, 865-875, 1991
A;Title: Complete sequence of the genes encoding the V(H) and V(L) regions of low- and h
patient.
A;Reference number: S23716; MUID:92031262; PMID:1718404
A;Accession: S23722
A;Molecule type: mRNA
A;Residues: 20-130 <HAW>
A;Cross-references: EMBL:X54438
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: immunoglobulin
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-130/Product: Ig lambda chain (fragment) #status predicted <MAT>
F;34-110/Domain: immunoglobulin homology <IMM>

  Query Match             81.4%;  Score 477;  DB 2;  Length 130;
  Best Local Similarity   80.2%;  Pred. No. 6e-34;
  Matches   89;  Conservative   10;  Mismatches   12;  Indels    0;  Gaps    0;

Qy          1 QSVLTQPPSVSAAPGQKVTISCSGSSSNIGNNFVSWYQQLPGTAPXLLIYDITKRPSGIP 60
              ||||||||| |  |||:|||||||||||||:|:| ||||||||| ||||   :||||:|
Db         20 QSVLTQPPSASGTPGQRVTISCSGSSSNIGSNYVYWYQQLPGTAPKLLIYRNNQRPSGVP 79

Qy         61 DRFSGSKSGTSATLGITGLQTGDEADYYCXTWDSSLSAVVFGGGTKLTVLG 111
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Db         80 DRFSGSKSGTSASLAISGLRSEDEADYYCATWDDSLSAVIFGGGTKLTVLG 130


RESULT 15
A42193
Ig lambda chain (BJP-DIA) - human
N;Alternate names: amyloid fibril protein AL-DIA; Bence Jones protein; Ig lambda chain (
C;Species: Homo sapiens (man)
C;Date: 03-Mar-1994 #sequence_revision 07-Apr-1994 #text_change 21-Jan-2000
C;Accession: A42193; S18297
R;Klafki, H.W.; Kratzin, H.D.; Pick, A.I.; Eckart, K.; Karas, M.; Hilschmann, N.
Biochemistry 31, 3265-3272, 1992
A;Title: Complete amino acid sequence determinations demonstrate identity of the urinary
A;Reference number: A42193; MUID:92207944; PMID:1554711
A;Accession: A42193
A;Molecule type: protein
A;Residues: 1-216 <KLA>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin; pyroglutamic acid
F;131-199/Domain: immunoglobulin homology <IMM>
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

  Query Match             80.9%;  Score 474;  DB 2;  Length 216;
  Best Local Similarity   77.2%;  Pred. No. 1.8e-33;
  Matches   88;  Conservative   11;  Mismatches   15;  Indels    0;  Gaps    0;

Qy          1 QSVLTQPPSVSAAPGQKVTISCSGSSSNIGNNFVSWYQQLPGTAPXLLIYDITKRPSGIP 60
              |||||||||  |  |||:|||||||||||||:| |:||||||||| ||||   :||||:|
Db          1 QSVLTQPPSASGTPGQRVTISCSGSSSNIGSNVVTWYQQLPGTAPKLLIYTNNQRPSGVP 60

Qy         61 DRFSGSKSGTSATLGITGLQTGDEADYYCXTWDSSLSAVVFGGGTKLTVLGQPK 114
               ||||||||||:| ::|||: ||||||| ||| |::  ||||||||||||||
Db         61 GRFSGSKSGTSASLAVSGLQSEDEADYYCATWDDSVNGWVFGGGTKLTVLGQPK 114


Search completed: October 13, 2005, 03:11:47
Job time : 24.485 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: October 13, 2005, 02:44:40 ; Search time 117.425 Seconds
(without alignments)
375.480 Million cell updates/sec

Title: US-10-010-729A-9
Perfect score: 586
Sequence: 1 QSVLTQPPSVSAAPGQKVTI.....SLSAVVFGGGTKLTVLGQPK 114

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	582	99.3	114	5	ABB07187	Abb07187 sHigM22 l
2	582	99.3	114	5	ABB07170	Abb07170 sHigM22 l
3	582	99.3	114	8	ADI26656	Adi26656 Human ant
4	547.5	93.4	234	8	ABM84293	Abm84293 Human dia
5	544	92.8	234	6	ABG73422	Abg73422 Human IgG
6	543	92.7	111	8	ABG75338	Abg75338 Antibody
7	539	92.0	234	7	AAE39158	Aae39158 IgG3 anti
8	539	92.0	248	8	ADS09288	Ads09288 Human c-M
9	538	91.8	111	2	AAR12263	Aar12263 Anti-huma
10	538	91.8	243	6	AAO31147	Aao31147 Human CM0
11	537.5	91.7	234	8	ABM84291	Abm84291 Human dia
12	537	91.6	110	8	ADP22405	Adp22405 Human ant
13	537	91.6	110	8	ADP22403	Adp22403 Human ant
14	534	91.1	258	5	ABP45249	Abp45249 Human BLy
15	534	91.1	258	7	ADG96076	Adg96076 Single ch
16	533	91.0	248	5	ABP45235	Abp45235 Human BLy
17	533	91.0	248	7	ADG96062	Adg96062 Single ch
18	532	90.8	112	6	ABR55778	Abr55778 Lambda ch
19	530	90.4	255	5	ABP45145	Abp45145 Human BLy
20	530	90.4	255	7	ADG95972	Adg95972 Single ch
21	528.5	90.2	212	8	ABM84288	Abm84288 Human dia
22	528	90.1	108	5	AAO18432	Aao18432 Anti-GD2
23	528	90.1	110	8	ADP22258	Adp22258 Human ant
24	528	90.1	110	8	ADP22180	Adp22180 Human ant
25	528	90.1	248	5	ABP44850	Abp44850 Human BLy
26	528	90.1	248	7	ADG95677	Adg95677 Single ch
27	528	90.1	248	8	ADS09259	Ads09259 Human c-M
28	528	90.1	251	5	ABP45540	Abp45540 Human BLy
29	528	90.1	251	7	ADG96367	Adg96367 Single ch
30	527.5	90.0	111	6	ABR55774	Abr55774 Lambda ch
31	526	89.8	111	5	AAO18430	Aao18430 Anti-GD2
32	526	89.8	253	5	ABP45848	Abp45848 Human BLy
33	526	89.8	253	7	ADG96675	Adg96675 Single ch
34	524	89.4	262	7	ADH44200	Adh44200 sFv antib
35	523	89.2	251	7	ADG30494	Adg30494 Human GMC
36	522	89.1	244	8	ADS09242	Ads09242 Human c-M
37	522	89.1	248	5	ABP45454	Abp45454 Human BLy
38	522	89.1	248	7	ADG96281	Adg96281 Single ch
39	522	89.1	248	8	ADG34302	Adg34302 Neurokini
40	522	89.1	251	5	ABP45527	Abp45527 Human BLy
41	522	89.1	251	7	ADG96354	Adg96354 Single ch
42	522	89.1	256	5	ABP45004	Abp45004 Human BLy
43	522	89.1	256	7	ADG95831	Adg95831 Single ch
44	521	88.9	109	5	AAO18435	Aao18435 Anti-GD2
45	521	88.9	123	6	AAO19680	Aao19680 P aerugin

ALIGNMENTS

RESULT 1
ABB07187
ID ABB07187 standard; protein; 114 AA.
XX
AC ABB07187;
XX
DT 13-MAR-2002 (first entry)
XX
DE sHigM22 light chain variable region clone II amino acid sequence.
XX
KW Neuromodulatory; central nervous system; CNS; sHIgM22; LYM 22; AKJR4;
KW ebvHigM MsI19D10; ebv HIgM CB2bG8; CB2iE12; CB2iE7; MSI19E5; virucide;
KW antiparkinsonian; neuroprotective; nootropic; vulnerary.
XX
OS Homo sapiens.
XX
PN WO200185797-A1.
XX
PD 15-NOV-2001.
XX
PF 30-MAY-2000; 2000WO-US014902.
XX
PR 10-MAY-2000; 2000US-00568351.
XX
PA (MAYO-) MAYO FOUND MEDICAL EDUCATION RES.
XX
PI Rodriguez M, Miller DJ, Pease LR;
XX
DR WPI; 2002-066596/09.
DR N-PSDB; ABA94244.
XX
PT Novel neuromodulatory agent (a human IgM monoclonal antibody), promoting
PT neurite outgrowth, regeneration, remyelination and neuroprotection in
PT central nervous system, useful to treat post-infectious
PT encephalomyelitis.
XX
PS Claim 23; Fig 18; 219pp; English.
XX
CC The invention provides a neuromodulatory agent (I) capable of promoting
CC neurite outgrowth, regeneration, remyelination and neuroprotection in
CC central nervous system (CNS). (I) is capable of inducing remyelination,
CC promoting cellular proliferation of glial cells, and promoting Ca2+
CC signaling with oligodendrocytes. An humanised antibody to (I) can be
CC selected from antibody sHIgM22 (LYM 22), ebvHigM MsI19D10, ebv HIgM
CC CB2bG8, AKJR4, CB2iE12, CB2iE7 or MSI19E5. (I) is useful for stimulating
CC remyelination of CNS axons, stimulating proliferation of glial cells in
CC CNS axons, or treating demyelinating disease of CNS in a mammal in need
CC of such therapy. (I) is capable of binding to structures and cells within

CC CNS. (I) is preferably useful for treating a demyelinating disease of CNS
CC of a mouse infected with Strain DA of Theiler's murine encephalomyelitis
CC (TMEV) or for treating a human being having multiple sclerosis, or a
CC human or domestic animal with a viral demyelinating disease, or a post-
CC neural disease of CNS. (I) is also useful for an in vitro method of
CC stimulating the proliferation of glial cells from mixed cell culture. (I)
CC is also useful for stimulating remyelination of CNS axons. The antibodies
CC are useful for preventing infection by a bacterium, virus or like
CC pathogen that causes demyelination or other neurodegenerative condition
CC in a subject. Methods where (I) is administered to a patient are useful
CC for treating multiple sclerosis, Parkinson's disease, Alzheimer's
CC disease, amyotrophic lateral sclerosis (ALS), a viral demyelinating
CC disease, CNS diseases, and other conditions in the CNS where nerves are
CC damaged as by trauma. The present sequence represents the sHigM22 light
CC chain variable region clone II amino acid sequence
XX
SQ Sequence 114 AA;

Query Match 99.3%; Score 582; DB 5; Length 114;
Best Local Similarity 98.2%; Pred. No. 8.8e-41;
Matches 112; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy          1 QSVLTQPPSVSAAPGQKVTISCSGSSSNIGNNFVSWYQQLPGTAPXLLIYDITKRPSGIP 60
              |||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Db          1 QSVLTQPPSVSAAPGQKVTISCSGSSSNIGNNFVSWYQQLPGTAPKLLIYDITKRPSGIP 60

Qy         61 DRFSGSKSGTSATLGITGLQTGDEADYYCXTWDSSLSAVVFGGGTKLTVLGQPK 114
              |||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db         61 DRFSGSKSGTSATLGITGLQTGDEADYYCETWDSSLSAVVFGGGTKLTVLGQPK 114
```

RESULT 2
ABB07170
ID ABB07170 standard; protein; 114 AA.
XX
AC ABB07170;
XX
DT 13-MAR-2002 (first entry)
XX
DE sHigM22 light chain variable region clone I amino acid sequence.
XX
KW Neuromodulatory; central nervous system; CNS; sHIgM22; LYM 22; AKJR4;
KW ebvHigM MsI19D10; ebv HIgM CB2bG8; CB2iE12; CB2iE7; MSI19E5; virucide;
KW antiparkinsonian; neuroprotective; nootropic; vulnerary.
XX
OS Homo sapiens.
XX
PN WO200185797-A1.
XX
PD 15-NOV-2001.
XX
PF 30-MAY-2000; 2000WO-US014902.
XX
PR 10-MAY-2000; 2000US-00568351.
XX
PA (MAYO-) MAYO FOUND MEDICAL EDUCATION RES.
XX
PI Rodriguez M, Miller DJ, Pease LR;
XX
DR WPI; 2002-066596/09.
DR N-PSDB; ABA94217.
XX
PT Novel neuromodulatory agent (a human IgM monoclonal antibody), promoting
PT neurite outgrowth, regeneration, remyelination and neuroprotection in
PT central nervous system, useful to treat post-infectious
PT encephalomyelitis.
XX
PS Claim 23; Fig 18; 219pp; English.
XX
CC The invention provides a neuromodulatory agent (I) capable of promoting
CC neurite outgrowth, regeneration, remyelination and neuroprotection in
CC central nervous system (CNS). (I) is capable of inducing remyelination,
CC promoting cellular proliferation of glial cells, and promoting Ca2+
CC signaling with oligodendrocytes. An humanised antibody to (I) can be
CC selected from antibody sHIgM22 (LYM 22), ebvHigM MsI19D10, ebv HIgM
CC CB2bG8, AKJR4, CB2iE12, CB2iE7 or MSI19E5. (I) is useful for stimulating
CC remyelination of CNS axons, stimulating proliferation of glial cells in
CC CNS axons, or treating demyelinating disease of CNS in a mammal in need
CC of such therapy. (I) is capable of binding to structures and cells within
CC CNS. (I) is preferably useful for treating a demyelinating disease of CNS
CC of a mouse infected with Strain DA of Theiler's murine encephalomyelitis
CC (TMEV) or for treating a human being having multiple sclerosis, or a
CC human or domestic animal with a viral demyelinating disease, or a post-
CC neural disease of CNS. (I) is also useful for an in vitro method of
CC stimulating the proliferation of glial cells from mixed cell culture. (I)
CC is also useful for stimulating remyelination of CNS axons. The antibodies
CC are useful for preventing infection by a bacterium, virus or like
CC pathogen that causes demyelination or other neurodegenerative condition
CC in a subject. Methods where (I) is administered to a patient are useful
CC for treating multiple sclerosis, Parkinson's disease, Alzheimer's
CC disease, amyotrophic lateral sclerosis (ALS), a viral demyelinating
CC disease, CNS diseases, and other conditions in the CNS where nerves are
CC damaged as by trauma. The present sequence represents the sHigM22 light
CC chain variable region clone I amino acid sequence
XX
SQ Sequence 114 AA;

Query Match 99.3%; Score 582; DB 5; Length 114;
Best Local Similarity 98.2%; Pred. No. 8.8e-41;
Matches 112; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy          1 QSVLTQPPSVSAAPGQKVTISCSGSSSNIGNNFVSWYQQLPGTAPXLLIYDITKRPSGIP 60
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Db          1 QSVLTQPPSVSAAPGQKVTISCSGSSSNIGNNFVSWYQQLPGTAPRLLIYDITKRPSGIP 60

Qy         61 DRFSGSKSGTSATLGITGLQTGDEADYYCXTWDSSLSAVVFGGGTKLTVLGQPK 114
              |||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db         61 DRFSGSKSGTSATLGITGLQTGDEADYYCGTWDSSLSAVVFGGGTKLTVLGQPK 114
```

RESULT 3
ADI26656
ID ADI26656 standard; protein; 114 AA.
XX
AC ADI26656;
XX
DT 15-APR-2004 (first entry)
XX
DE Human anti IgM antibody sHIgM22 VL protein.
XX
KW Human; antibody; IgM; remyelination; neuronal growth; autoantibody;
KW demyelination disease; multiple sclerosis; central nervous system; CNS;
KW axon; glial cell proliferation;
KW Theiler's murine encephalomyelitis virus infection; CNS injury;
KW spinal cord injury.
XX
OS Homo sapiens.
XX
PN US2003185827-A1.
XX
PD 02-OCT-2003.
XX
PF 13-NOV-2001; 2001US-00010729.
XX
PR 29-APR-1994; 94US-00236520.
PR 08-AUG-1996; 96US-00692084.
PR 07-JAN-1997; 97US-00779784.
PR 28-MAY-1999; 99US-00322862.
PR 30-MAY-2000; 2000US-00580787.
PR 05-DEC-2000; 2000US-00730473.
XX
PA (MAYO-) MAYO FOUND.
XX
PI Rodriguez M, Miller DJ, Pease LR;
XX
DR WPI; 2004-119219/12.

DR N-PSDB; ADI26657.
XX
PT New human immunoglobulin M antibody for treating or preventing a
PT demyelinating disease of the central nervous system in a human or
PT domestic animal, such as multiple sclerosis.
XX
PS Claim 6; Fig 36; 159pp; English.
XX
CC The invention relates to an antibody (I) produced by injecting an
CC immunocompetent host with an antibody peptide, and harvesting the
CC antibody, where the peptide comprises a human anti-IgM antibody fragment
CC given in the specification, or active fragments. Also included are
CC stimulating remyelination of central nervous system (CNS) axons in a
CC mammal (comprising administering a monoclonal antibody, or mixtures,
CC monomers, active fragments, or recombinant antibodies derived from it,
CC characterised by their ability to bind structures and cells within the
CC CNS, including oligodendrocytes), stimulating the proliferation of glial
CC cells in CNS axons in a mammal (comprising administering a monoclonal
CC antibody, or mixtures, monomers, active fragments, or recombinant
CC antibodies derived from it, characterised by their ability to bind
CC structures and cells within the CNS), treating or preventing a
CC demyelinating disease of the CNS in a mammal (comprising administering a
CC monoclonal antibody, or mixtures, monomers, active fragments, or
CC recombinant antibodies derived from it, characterised by their ability to
CC bind structures and cells within the CNS, and to stimulate remyelination
CC of axons of the CNS), stimulating, in vitro, the proliferation of glial
CC cells from mixed cell culture, stimulating remyelination of CNS axons in
CC a mammal, a DNA sequence (or degenerate variant of it) which encodes an
CC antibody(or a peptide analogue, hapten, or active fragment of it, where
CC the DNA sequence consists of a sequence encoding an anti IgM antibody), a
CC probe capable of screening for the antibody, an assay for screening drugs
CC and other agents for the ability to modulate the production or mimic the
CC activities of mAB sHIgM22, sHIgM46, or combinations of them, a
CC recombinant virus transformed with recombinant antibody nucleic acids or
CC vector, imaging a portion of the CNS using the antibody and diagnosing or
CC monitoring demyelination and/or remyelination of the CNS comprising using
CC CNS image. The antibody is used to stimulate remyelination of CNS axons,
CC and to stimulate the proliferation of glial cells in CNS axons,
CC optionally in vitro. The antibody is used to treat or prevent a
CC demyelinating disease of the CNS in a human or domestic animal, such as
CC multiple sclerosis, or a disease, other injury or dysfunction of the CNS,
CC preferably the mammal is a mouse infected with Strain DA of Theiler's
CC murine encephalomyelitis virus. The antibody is used to treat a spinal
CC cord injury and used to screen drugs and other agents for the ability to
CC modulate the production or mimic the activities of the antibody. The
CC antibody can be used to image a portion of the CNS which can be used to
CC diagnose or monitor demyelination and/or remyelination of the CNS. The
CC present sequence is a variable region of a human anti-IgM antibody (or
CC fragment).
XX
SQ Sequence 114 AA;

```
  Query Match             99.3%;  Score 582;  DB 8;  Length 114;
  Best Local Similarity   100.0%;  Pred. No. 8.8e-41;
  Matches  114;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 QSVLTQPPSVSAAPGQKVTISCSGSSSNIGNNFVSWYQQLPGTAPXLLIYDITKRPSGIP 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 QSVLTQPPSVSAAPGQKVTISCSGSSSNIGNNFVSWYQQLPGTAPXLLIYDITKRPSGIP 60

Qy         61 DRFSGSKSGTSATLGITGLQTGDEADYYCXTWDSSLSAVVFGGGTKLTVLGQPK 114
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 DRFSGSKSGTSATLGITGLQTGDEADYYCXTWDSSLSAVVFGGGTKLTVLGQPK 114
```

RESULT 4
ABM84293
ID ABM84293 standard; protein; 234 AA.
XX
AC ABM84293;
XX
DT 18-NOV-2004 (first entry)
XX
DE Human diagnostic and therapeutic pprotein SEQ ID NO:4542.
XX
KW gene therapy; human diagnostic and therapeutic polynucleotide; dithp.
XX
OS Homo sapiens.
XX
PN WO2004023973-A2.
XX
PD 25-MAR-2004.
XX
PF 12-SEP-2003; 2003WO-US028227.
XX
PR 12-SEP-2002; 2002US-0410259P.
PR 12-SEP-2002; 2002US-0410260P.
XX
PA (INCY-) INCYTE CORP.
XX
PI Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F;
PI Harthshorne TA, Suchorolski MT, Altus CM, Pitts SJ, Elder LV;
PI Mooney EM, Delegeane AM, Panesar IS, Banville SC, Reddy TP;
PI Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstin EH;
PI Peralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LL;
PI Lagace RE, Spiro PA, Stewart EA, Wingrove J, Vitt UA, Kirton ES;
PI Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D;
PI Patury S, Shi X, Suarez CJ;
XX
DR WPI; 2004-329368/30.
DR N-PSDB; ACN42945.
XX
PT New diagnostic and therapeutic polynucleotides and polypeptides, useful
PT in diagnosing a condition, disease or disorder associated with human
PT molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or
PT in gene mapping.
XX
PS Claim 27; Page; 190pp; English.
XX
CC The invention relates to novel diagnostic and therapeutic polynucleotides
CC selected from one of the 2722 sequences defined in the specification. A
CC polynucleotide of the invention may have a use in gene therapy. The human
CC diagnostic and therapeutic polynucleotides (dithp) or polypeptides may be
CC used to diagnose a particular condition, disease or disorder associated
CC with human molecules, e.g. cell proliferative disorders,
CC autoimmune/inflammatory disorder, developmental disorder, endocrine
CC disorder, neurological disorders, gastrointestinal disorders, or
CC infections caused by virus, bacteria, fungi or parasite. The dithp
CC molecules may also be used in genetic mapping, in identifying individuals
CC from minute biological samples, in detecting single nucleotide
CC polymorphisms, as molecular weight markers, and for somatic or germline
CC gene therapy. The present sequence represents a dithp protein of the
CC invention. Note: The sequence data for this patent is not represented in
CC the printed specification, but was obtained in electronic format directly
CC from WIPO at www.wipo.int/pct/en/sequences/listing.htm
XX
SQ Sequence 234 AA;

```
  Query Match             93.4%;  Score 547.5;  DB 8;  Length 234;
  Best Local Similarity   93.9%;  Pred. No. 1.3e-37;
  Matches  107;  Conservative    1;  Mismatches    5;  Indels    1;  Gaps    1;

Qy          1 QSVLTQPPSVSAAPGQKVTISCSGSSSNIGNNFVSWYQQLPGTAPXLLIYDITKRPSGIP 60
              ||||||||||||||||||||||||||||||:||||||||||| |||||  |||||||
Db         20 QSVLTQPPSVSAAPGQKVTISCSGSSSNIGNNYVSWYQQLPGTAPKLLIYDNNKRPSGIP 79

Qy         61 DRFSGSKSGTSATLGITGLQTGDEADYYCXTWDSSLSAVVFGGGTKLTVLGQPK 114
              |||||||||||||||||||||||||||| ||||||  ||||||||||||||||
Db         80 DRFSGSKSGTSATLGITGLQTGDEADYYCGTWDSSL-MVVFGGGTKLTVLGQPK 132
```

RESULT 5
ABG73422
ID ABG73422 standard; protein; 234 AA.
XX
AC ABG73422;

```
XX
DT   24-APR-2003  (first entry)
XX
DE   Human IgG anti-rhesus antibody lambda light chain polypeptide.
XX
KW   IgG anti-rhesus antibody; Rh; gamma 3 heavy chain; lambda light chain;
KW   haemagglutinin; rhesus antigen; red blood cell; agglutination; antibody;
KW   Rh phenotyping; human.
XX
OS   Homo sapiens.
XX
PN   US6475749-B1.
XX
PD   05-NOV-2002.
XX
PF   11-AUG-1999;   99US-00372425.
XX
PR   11-AUG-1999;   99US-00372425.
XX
PA   (REGC ) UNIV CALIFORNIA.
XX
PI   Morrison SL,  Montano R;
XX
DR   WPI; 2003-208833/20.
DR   N-PSDB; ABX15392.
XX
PT   Reagent for identifying rhesus antigen on red blood cells, comprises Rh
PT   antibody hybrid having IgG anti-Rh antibody which has polymeric tail
PT   piece attached to carboxy terminal end of each of IgG antibody heavy
PT   chains.
XX
PS   Claim 1; Col 13-16; 14pp; English.
XX
CC   The invention relates to a reagent comprising an IgG anti-Rh antibody
CC   having two lambda light chains, two gamma 3 heavy chains and a polymeric
CC   tailpiece attached to the carboxy terminal end of the heavy chain. The
CC   reagent is useful in a haemagglutinin test to determine the presence of
CC   one or more Rh (rhesus) antigens on red blood cells. The reagent is also
CC   useful for testing red blood cells to determine the presence of one or
CC   more Rh factors, by contacting red blood cells with the reagent for a
CC   sufficient time and at a sufficient temperature to cause agglutination of
CC   red blood cells which have one or more Rh factors present, and
CC   determining whether the red blood cells agglutinate to determine the
CC   presence of one or more Rh factors. The reagent allows fast and accurate
CC   Rh phenotyping of blood and is used in the one-step haemagglutinin
CC   method. This sequence represents a human IgG anti-Rh antibody lambda
CC   light chain polypeptide
XX
SQ   Sequence 234 AA;

  Query Match             92.8%;  Score 544;  DB 6;  Length 234;
  Best Local Similarity   90.4%;  Pred. No. 2.5e-37;
  Matches  103;  Conservative    5;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 QSVLTQPPSVSAAPGQKVTISCSGSSSNIGNNFVSWYQQLPGTAPXLLIYDITKRPSGIP 60
              ||||||||||||||||||||||||||||||:|||||  ||||| |||||  :||||||
Db         19 QSVLTQPPSVSAAPGQKVTISCSGSSSNIGNNYVSWYQHFPGTAPKLLIYDNNQRPSGIP 78

Qy         61 DRFSGSKSGTSATLGITGLQTGDEADYYCXTWDSSLSAVVFGGGTKLTVLGQPK 114
              |||||||||||||||||||||||||||| |||||||||:|||||::|||||||
Db         79 DRFSGSKSGTSATLGITGLQTGDEADYYCGTWDSSLSAVLFGGGTEVTVLGQPK 132


RESULT 6
ABG75338
ID   ABG75338 standard; protein; 111 AA.
XX
AC   ABG75338;
XX
DT   22-APR-2004  (first entry)
XX
DE   Antibody single chain framework polypeptide SEQ ID NO: 4.
XX
KW   Antibody; framework; stability; intracellular; Fv; solubility.
XX
OS   Synthetic.
XX
PN   WO2003097697-A2.
XX
PD   27-NOV-2003.
XX
PF   21-MAY-2003; 2003WO-EP005324.
XX
PR   22-MAY-2002; 2002US-0382649P.
PR   03-JAN-2003; 2003US-0438256P.
XX
PA   (ESBA-) ESBATECH AG.
XX
PI   Tissot K,  Ewert S,  Auf Der Maur A,  Barberis A,  Escher D;
XX
DR   WPI; 2004-022852/02.
XX
PT   New single chain immunoglobulin frameworks that demonstrate enhanced
PT   stability in the intracellular environment, useful for target validation,
PT   library construction, or in therapeutic or diagnostic applications.
XX
PS   Claim 6; Page 48; 0pp; English.
XX
CC   The present invention relates to a single chain antibody framework. The
CC   single chain framework, antibody or antibody fragment, is useful in
CC   target validation, diagnostic applications, library construction or
CC   therapeutic applications. The framework sequences are used in the
CC   identification of a conserved framework residue class selected from polar
CC   but uncharged R groups, positively charged R groups, negatively charged R
CC   groups, hydrophobic R groups, and special amino acids. The framework
CC   sequences may also be used in the identification of at least one
CC   conserved framework sequence, where the conserved framework sequence is 2
CC   -5, 5-10 or 10-25 residues, and where the conserved framework sequence
CC   has gaps. The nucleic acid molecule is used in gene therapy. The present
CC   sequence is a polypeptide of the invention
XX
SQ   Sequence 111 AA;

  Query Match             92.7%;  Score 543;  DB 8;  Length 111;
  Best Local Similarity   93.7%;  Pred. No. 1.5e-37;
  Matches  104;  Conservative    3;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 QSVLTQPPSVSAAPGQKVTISCSGSSSNIGNNFVSWYQQLPGTAPXLLIYDITKRPSGIP 60
              |||||||||||||||||||||||||||||:||||:|:|||||||||||| ||||| ||||||||
Db          1 QSVLTQPPSVSAAPGQKVTISCSGSTSNIGDNYVSWYQQLPGTAPQLLIYDNTKRPSGIP 60

Qy         61 DRFSGSKSGTSATLGITGLQTGDEADYYCXTWDSSLSAVVFGGGTKLTVLG 111
              ||||||||||||||||||||||||||||| ||||||| |||||||||||||
Db         61 DRFSGSKSGTSATLGITGLQTGDEADYYCGTWDSSLSGVVFGGGTKLTVLG 111


RESULT 7
AAE39158
ID   AAE39158 standard; protein; 234 AA.
XX
AC   AAE39158;
XX
DT   18-DEC-2003  (first entry)
XX
DE   IgG3 antibody lambda light chain protein.
XX
KW   Anti-rhesus antibody; Rh; immunoglobulin G; IgG; haemagglutinin test;
KW   Rh phenotyping; therapeutic; haemolytic disease; Rh incompatibility;
KW   prophylactic.
XX
OS   Unidentified.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 111
FT                   /note= "Encoded by GAT"
XX
```

PN US2003143643-A1.
XX
PD 31-JUL-2003.
XX
PF 12-JUL-2002; 2002US-00194801.
XX
PR 11-AUG-1999; 99US-00372425.
XX
PA (REGC) UNIV CALIFORNIA.
XX
PI Morrison SL, Montano R;
XX
DR WPI; 2003-755510/71.
DR N-PSDB; AAD59473.
XX
PT Hybrid immunoglobulin G anti-Rhesus antibody for use in one-step Rh
PT phenotyping of blood or as a prophylactic agent to prevent hemolytic
PT disease in newborns due to Rh incompatibility, comprises a polymeric
PT carboxy terminus tailpiece.
XX
PS Claim 7; Page 8-9; 0pp; English.
XX
CC The invention relates to hybrid anti-Rhesus (Rh) antibody comprising an
CC immunoglobulin (Ig)G anti-Rh antibody which comprises two light chains
CC and two heavy chains where the heavy chains have a carboxy terminal with
CC a polymeric tailpiece and an amino terminal. The antibodies are used in a
CC one-step haemagglutinin test to provide Rh phenotyping of blood and as
CC therapeutic or prophylactic agents for preventing haemolytic disease in
CC newborns due to Rh incompatibility. The present sequence is IgG3 antibody
CC lambda light chain protein
XX
SQ Sequence 234 AA;

Query Match 92.0%; Score 539; DB 7; Length 234;
Best Local Similarity 89.5%; Pred. No. 6.6e-37;
Matches 102; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

```
Qy          1 QSVLTQPPSVSAAPGQKVTISCSGSSSNIGNNFVSWYQQLPGTAPXLLIYDITKRPSGIP 60
              ||||||||||||||||||||||||||||||:|||||  ||||| |||||  :||||||
Db         19 QSVLTQPPSVSAAPGQKVTISCSGSSSNIGNNYVSWYQHFPGTAPKLLIYDNNQRPSGIP 78

Qy         61 DRFSGSKSGTSATLGITGLQTGDEADYYCXTWDSSLSAVVFGGGTKLTVLGQPK 114
              |||||||||||||||||||||||||||| ||:||||||:|||||::|||||||
Db         79 DRFSGSKSGTSATLGITGLQTGDEADYYCGTWNSSLSAVLFGGGTEVTVLGQPK 132
```

RESULT 8
ADS09288
ID ADS09288 standard; protein; 248 AA.
XX
AC ADS09288;
XX
DT 18-NOV-2004 (first entry)
XX
DE Human c-Met protein tyrosine kinase antibody, PGIA-4-A3.
XX
KW c-Met; tyrosine kinase antibody; antigen binding; cytostatic;
KW ophthalmological; antiinflammatory; analgesic; vasotropic; antipsoriatic;
KW osteopathic; cancer; tumour; ophthalmic disease; glaucoma; retinitis;
KW retinopathy; uveitis; ocular photophobia; macular degeneration; pain;
KW acute injury; eye; hyperproliferative disorder; restenosis; angioplasty;
KW psoriasis; HGF; osteoporosis; cancer.
XX
OS Homo sapiens.
XX
PN WO2004072117-A2.
XX
PD 26-AUG-2004.
XX
PF 11-FEB-2004; 2004WO-IB000503.
XX
PR 13-FEB-2003; 2003US-0447073P.
XX
PA (PHAA) PHARMACIA CORP.
XX
PI Morton PA, Arbuckle JA, Evans ML, Joy WD, Kahn LE, Shieh JJ;
XX
DR WPI; 2004-616044/59.
DR N-PSDB; ADS09348.
XX
PT Novel c-Met protein tyrosine kinase antibody or its antigen-binding
PT portion specifically binding to c-Met, useful for manufacture of
PT medicament for treating cancer or tumor and for treatment of ophthalmic
PT diseases such as glaucoma.
XX
PS Claim 1; SEQ ID NO 50; 303pp; English.
XX
CC The invention relates to a novel c-Met protein tyrosine kinase antibody
CC or its antigen binding portion that specifically binds to c-Met. The c-
CC Met antibody comprises any one of 1-60 fully defined sequence of 238,
CC 244, 240, 250, 251, 242, 245, 247, 246, 253, 249, 243, 241, etc., amino
CC acids as given in the specification, or its fragment. The invention
CC further comprises: a pharmaceutical composition comprising the c-Met
CC protein tyrosine kinase antibody and a carrier; an isolated cell that
CC produces the c-Met protein tyrosine kinase antibody; and an isolated
CC nucleic acid molecule that comprises a nucleic acid sequence that encodes
CC a heavy chain or its antigen-binding portion or light chain or its
CC antigen-binding portion of the c-Met protein tyrosine kinase antibody.
CC The c-Met protein tyrosine kinase antibody has cytostatic,
CC ophthalmological, antiinflammatory, analgesic, vasotropic, antipsoriatic,
CC and osteopathic activities. The c-Met protein tyrosine kinase antibody is
CC useful for the manufacture of medicament for the treatment of cancer or
CC tumour. The c-Met protein tyrosine kinase antibody is useful for
CC diagnosing the presence or ligation of c-Met expressing tissue. The c-Met
CC protein tyrosine kinase antibody is useful for detecting c-Met in a
CC biological sample in vitro or in vivo. The c-Met protein tyrosine kinase
CC antibody is also useful in the treatment or prevention of ophthalmic
CC diseases such as glaucoma, retinitis, retinopathies (e.g., diabetic
CC retinopathy), uveitis, ocular photophobia, macular degeneration and pain
CC associated with acute injury to the eye. The pharmaceutical composition
CC is useful for the treatment of hyperproliferative disorders such as
CC restenosis after angioplasty, and psoriasis, and for the treatment of
CC animals that lack sufficient HGF, e.g. osteoporosis and cancer. This
CC sequence represents the protein of a phage display generated human c-Met
CC antibody of the invention.
XX
SQ Sequence 248 AA;

Query Match 92.0%; Score 539; DB 8; Length 248;
Best Local Similarity 92.8%; Pred. No. 7e-37;
Matches 103; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

```
Qy          1 QSVLTQPPSVSAAPGQKVTISCSGSSSNIGNNFVSWYQQLPGTAPXLLIYDITKRPSGIP 60
              |||:|||||||||||||||||||||||||||:||||:||||||| |||||  |||||||
Db        138 QSVVTQPPSVSAAPGQKVTISCSGSSSNIGNNYVSWYKQLPGTAPKLLIYDNNKRPSGIP 197

Qy         61 DRFSGSKSGTSATLGITGLQTGDEADYYCXTWDSSLSAVVFGGGTKLTVLG 111
              |||||||||||||||||||||||||||| ||||||| ||||||||||||
Db        198 DRFSGSKSGTSATLGITGLQTGDEADYYCGTWDSSLSGVVFGGGTKLTVLG 248
```

RESULT 9
AAR12263
ID AAR12263 standard; protein; 111 AA.
XX
AC AAR12263;
XX
DT 25-MAR-2003 (revised)
DT 15-AUG-1991 (first entry)
XX
DE Anti-human RhD FOG-B MAb (VL chain).
XX
KW Monoclonal antibody; rhesus D; blood-typing; CDR;
KW haemolytic disease of the newborn; HDN.
XX
OS Homo sapiens.

```
XX
FH   Key             Location/Qualifiers
FT   Region          23. .35
FT                   /label= CDR1
FT   Region          51. .57
FT                   /label= CDR2
FT   Region          90. .100
FT                   /label= CDR3
XX
PN   WO9107492-A.
XX
PD   30-MAY-1991.
XX
PF   13-NOV-1989;   89GB-00025590.
XX
PR   13-NOV-1989;   89GB-00025590.
XX
PA   (BLOO-) CENT BLOOD LAB AUTHORITY.
XX
PI   Hughesjone N;
XX
DR   WPI; 1991-178104/24.
DR   N-PSDB; AAQ11945.
XX
PT   DNA encoding complementary determining regions - of human anti-rhesus d
PT   antibodies, useful in prodn. of monoclonal antibodies and for passive
PT   immunisation.
XX
PS   Disclosure; Fig 2; 32pp; English.
XX
CC   The DNA sequence of eleven monoclonal antibodies are represented in
CC   Q119145-57. Synthetic genes, for both heavy and light chains may be
CC   created by combining selected CDR 1, 2, and 3 regions, which may be
CC   selected from different antibody mols. having varied binding specificity.
CC   The chimaeric anti-RhD antibodies can be used for diagnosis and therapy,
CC   and are capable of providing blood- typing reagents of high specificity
CC   and reliability. They can also be used in passive immunisation to prevent
CC   haemolytic disease of the newborn. (Updated on 25-MAR-2003 to correct PA
CC   field.) (Updated on 25-MAR-2003 to correct PI field.)
XX
SQ   Sequence 111 AA;

  Query Match             91.8%;  Score 538;  DB 2;  Length 111;
  Best Local Similarity   93.6%;  Pred. No. 3.8e-37;
  Matches  103;  Conservative    3;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 QSVLTQPPSVSAAPGQKVTISCSGSSSNIGNNFVSWYQQLPGTAPXLLIYDITKRPSGIP 60
              ||||||||||||||||||||||||:|||||||:||||||||||| |||||  |||||||
Db          1 QSVLTQPPSVSAAPGQKVTISCSGTSSNIGNNYVSWYQQLPGTAPKLLIYDNNKRPSGIP 60

Qy         61 DRFSGSKSGTSATLGITGLQTGDEADYYCXTWDSSLSAVVFGGGTKLTVL 110
              ||||||||||||||||||:||||||||| ||||||||||||||||||||
Db         61 DRFSGSKSGTSATLGITGLRTGDEADYYCATWDSSLSAVVFGGGTKLTVL 110


RESULT 10
AAO31147
ID   AAO31147 standard; protein; 243 AA.
XX
AC   AAO31147;
XX
DT   06-OCT-2003  (first entry)
XX
DE   Human CM085C11 scFv protein that specifically binds TR7.
XX
KW   Human; protein coordinate data; heavy chain variable domain; VH; cancer;
KW   complementarity determining region; CDR; light chain variable domain; VL;
KW   TRAIL receptor 7; TR7; tumour necrosis factor; KILLER; death receptor 5;
KW   DR5; TRAIL receptor 2; TRAIL-R2; TNF-related apoptosis-inducing ligand;
KW   Kaposi's sarcoma; central nervous system; medulloblastoma; neuroblastoma;
KW   glioblastoma; graft versus host disease; antibody therapy; nootropic;
KW   AIDS; acquired immune deficiency syndrome; neurodegenerative disorder;
KW   immunosuppressive; neuroprotective; antibody therapy; antibody.
XX
OS   Homo sapiens.
XX
PN   WO2003054216-A2.
XX
PD   03-JUL-2003.
XX
PF   19-DEC-2002; 2002WO-US040597.
XX
PR   20-DEC-2001; 2001US-0341237P.
PR   05-APR-2002; 2002US-0369877P.
PR   04-JUN-2002; 2002US-0384828P.
PR   18-JUL-2002; 2002US-0396591P.
PR   15-AUG-2002; 2002US-0403370P.
PR   13-NOV-2002; 2002US-0425737P.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
XX
PI   Salcedo T,  Albert VR,  Rosen CA,  Humphreys R,  Vaughan TJ;
XX
DR   WPI; 2003-569250/53.
DR   N-PSDB; AAL62844.
XX
PT   New antibody or its fragment, useful for treating, preventing or
PT   ameliorating a cancer, e.g. colon, breast, uterine, pancreatic, lung or
PT   gastrointestinal cancer, or Kaposi's sarcoma or, graft versus host
PT   disease, AIDS.
XX
PS   Claim 2; Page 288; 301pp; English.
XX
CC   The invention relates to an isolated antibody or its fragments such as
CC   VHCDR1 (heavy chain variable domain complementarity determining region),
CC   VHCDR2, VHCDR3, VLCDR1 (light chain variable domain complementarity
CC   determining region), VLCDR2 or VLCDR3. The antibody or its fragment
CC   immunospecifically binds TRAIL (tumour necrosis factor; TNF-related
CC   apoptosis-inducing ligand) receptor 7 (TR7). TR7 is also referred to as
CC   TRAIL receptor 2 (TRAIL-R2), death receptor 5 (DR5) and KILLER. The
CC   antibody or its fragment is useful for treating, preventing or
CC   ameliorating a cancer, e.g. colon, breast, uterine, pancreatic, lung or
CC   gastrointestinal cancer or Kaposi's sarcoma or cancer of the central
CC   nervous system such as medulloblastoma, neuroblastoma or glioblastoma or
CC   graft versus host disease, AIDS (acquired immune deficiency syndrome) or
CC   a neurodegenerative disorder. The invention is useful in antibody
CC   therapy. The present sequence is human scFv protein that specifically
CC   binds TR7
XX
SQ   Sequence 243 AA;

  Query Match             91.8%;  Score 538;  DB 6;  Length 243;
  Best Local Similarity   91.9%;  Pred. No. 8.3e-37;
  Matches  102;  Conservative    5;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 QSVLTQPPSVSAAPGQKVTISCSGSSSNIGNNFVSWYQQLPGTAPXLLIYDITKRPSGIP 60
              ||||||||||||||||||||||||:||||||:||||||:||||| |||||  |||||||
Db        133 QSVLTQPPSVSAAPGQKVTISCSGSTSNIGNNYVSWYQQVPGTAPKLLIYDNNKRPSGIP 192

Qy         61 DRFSGSKSGTSATLGITGLQTGDEADYYCXTWDSSLSAVVFGGGTKLTVLG 111
              |||||||||||||||||||||||||||| ||||||||:|||||||:||||
Db        193 DRFSGSKSGTSATLGITGLQTGDEADYYCGTWDSSLSALVFGGGTKVTVLG 243


RESULT 11
ABM84291
ID   ABM84291 standard; protein; 234 AA.
XX
AC   ABM84291;
XX
DT   18-NOV-2004  (first entry)
XX
DE   Human diagnostic and therapeutic pprotein SEQ ID NO:4540.
XX
KW   gene therapy; human diagnostic and therapeutic polynucleotide; dithp.
XX
```

OS Homo sapiens.
XX
PN WO2004023973-A2.
XX
PD 25-MAR-2004.
XX
PF 12-SEP-2003; 2003WO-US028227.
XX
PR 12-SEP-2002; 2002US-0410259P.
PR 12-SEP-2002; 2002US-0410260P.
XX
PA (INCY-) INCYTE CORP.
XX
PI Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F;
PI Harthshorne TA, Suchorolski MT, Altus CM, Pitts SJ, Elder LV;
PI Mooney EM, Delegeane AM, Panesar IS, Banville SC, Reddy TP;
PI Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstin EH;
PI Peralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LL;
PI Lagace RE, Spiro PA, Stewart EA, Wingrove J, Vitt UA, Kirton ES;
PI Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D;
PI Patury S, Shi X, Suarez CJ;
XX
DR WPI; 2004-329368/30.
DR N-PSDB; ACN42943.
XX
PT New diagnostic and therapeutic polynucleotides and polypeptides, useful
PT in diagnosing a condition, disease or disorder associated with human
PT molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or
PT in gene mapping.
XX
PS Claim 27; Page; 190pp; English.
XX
CC The invention relates to novel diagnostic and therapeutic polynucleotides
CC selected from one of the 2722 sequences defined in the specification. A
CC polynucleotide of the invention may have a use in gene therapy. The human
CC diagnostic and therapeutic polynucleotides (dithp) or polypeptides may be
CC used to diagnose a particular condition, disease or disorder associated
CC with human molecules, e.g. cell proliferative disorders,
CC autoimmune/inflammatory disorder, developmental disorder, endocrine
CC disorder, neurological disorders, gastrointestinal disorders, or
CC infections caused by virus, bacteria, fungi or parasite. The dithp
CC molecules may also be used in genetic mapping, in identifying individuals
CC from minute biological samples, in detecting single nucleotide
CC polymorphisms, as molecular weight markers, and for somatic or germline
CC gene therapy. The present sequence represents a dithp protein of the
CC invention. Note: The sequence data for this patent is not represented in
CC the printed specification, but was obtained in electronic format directly
CC from WIPO at www.wipo.int/pct/en/sequences/listing.htm
XX
SQ Sequence 234 AA;

Query Match 91.7%; Score 537.5; DB 8; Length 234;
Best Local Similarity 92.1%; Pred. No. 8.8e-37;
Matches 105; Conservative 2; Mismatches 6; Indels 1; Gaps 1;

```
Qy          1 QSVLTQPPSVSAAPGQKVTISCSGSSSNIGNNFVSWYQQLPGTAPXLLIYDITKRPSGIP 60
              ||||||||||||||||||||||||||||||:|||||||||||| |||||  |||||||
Db         20 QSVLTQPPSVSAAPGQKVTISCSGSSSNIGNNYVSWYQQLPGTAPKLLIYDNNKRPSGIP 79

Qy         61 DRFSGSKSGTSATLGITGLQTGDEADYYCXTWDSSLSAVVFGGGTKLTVLGQPK 114
              |||||||||||||||||||||||||||| ||||||  : |||||||||||||||
Db         80 DRFSGSKSGTSATLGITGLQTGDEADYYCGTWDSSL-MLGFGGGTKLTVLGQPK 132
```

RESULT 12
ADP22405
ID ADP22405 standard; protein; 110 AA.
XX
AC ADP22405;
XX
DT 09-SEP-2004 (first entry)
XX
DE Human anti-TNFa antibody light chain variable region SEQ ID NO:311.
XX
KW human; monoclonal antibody; tumour necrosis factor-alpha; TNFa;
KW anti-TNFa antibody; anabolic; antiarteriosclerotic; antiarthritic;
KW antibacterial; antiinflammatory; antipsoriatic; antirheumatic;
KW eating-disorder; immunomodulator; immunosuppressive; nephrotropic;
KW neuroprotective; vasotropic; antiapoptotic; TNFa antagonist;
KW TNF induced apoptosis; neoplastic disease; breast cancer; ovarian cancer;
KW bladder cancer; lung cancer; glioblastoma; stomach cancer;
KW endometrial cancer; kidney cancer; colon cancer; pancreatic cancer;
KW prostrate cancer; immuno-mediated inflammatory disease;
KW rheumatoid arthritis; glomerulonephritis; atherosclerosis; psoriasis;
KW restenosis; autoimmune disease; Crohn's disease; graft-host reaction;
KW septic shock; cachexia; anorexia; multiple sclerosis.
XX
OS Homo sapiens.
XX
PN WO2004050683-A2.
XX
PD 17-JUN-2004.
XX
PF 02-DEC-2003; 2003WO-US038281.
XX
PR 02-DEC-2002; 2002US-0430729P.
XX
PA (ABGE-) ABGENIX INC.
XX
PI Babcook JS, Kang JS, Foord O, Green L, Peng X, Klakamp S;
PI Haak-Frendscho M, Rathanaswami P, Pigott C, Liang ML, Lee R;
PI Manchulencho K, Paggioni R, Senaldi G, Qiaojuan JS;
XX
DR WPI; 2004-480601/45.
XX
PT New recombinant human monoclonal antibody that specifically binds to
PT Tumor Necrosis Factor-alpha, useful for treating neoplastic disease such
PT as cancers, or immuno-mediated inflammatory diseases such as rheumatoid
PT arthritis.
XX
PS Example 10; SEQ ID NO 311; 213pp; English.
XX
CC The present invention describes a human monoclonal antibody (I) that
CC specifically binds to tumour necrosis factor-alpha (TNFa) and comprises:
CC (a) a heavy chain complementarity determining region 1 (CDR1) having the
CC two fully defined 5 amino acid sequence (S1, ADP22417) or (S2, ADP22421);
CC and (b) a light chain CDR1 having the two fully defined 11 amino acid
CC sequence (S3, ADP22418) or (S4, ADP22424). Also described: (1) assaying
CC (M1) the level of TNFa in a patient sample, comprising contacting with
CC (I), and detecting the level of binding between the antibody and TNFa in
CC the sample; (2) a composition comprising the antibody or its functional
CC fragment and a carrier; (3) treating (M2) an animal suffering from a
CC neoplastic, or an immuno-mediated inflammatory disease by selecting an
CC animal in need of treatment for the disease by administering the human
CC monoclonal antibody of (I); and (4) inhibiting (M3) TNFa induced
CC apoptosis in an animal by selecting an animal in need of treatment for
CC TNFa induced apoptosis by administering the human monoclonal antibody of
CC (I). (I) has anabolic, antiarteriosclerotic, antiarthritic,
CC antibacterial, antiinflammatory, antipsoriatic, antirheumatic, eating-
CC disorders, immunomodulator, immunosuppressive, nephrotropic,
CC neuroprotective, vasotropic and antiapoptotic activities, and can be used
CC as a TNFa antagonist. The antibody (I) is useful in the preparation of
CC medicament for treating TNF induced apoptosis, neoplastic disease such as
CC breast cancer, ovarian cancer, bladder cancer, lung cancer, glioblastoma,
CC stomach cancer, endometrial cancer, kidney cancer, colon cancer,
CC pancreatic cancer, and prostrate cancer; or immuno-mediated inflammatory
CC diseases such as rheumatoid arthritis, glomerulonephritis,
CC atherosclerosis, psoriasis, restenosis, autoimmune disease, Crohn's
CC disease, graft-host reactions, septic shock, cachexia, anorexia, and
CC multiple sclerosis. The present sequence represents a human anti-TNFa
CC antibody light chain variable region, which is used in the
CC exemplification of the present invention.
XX
SQ Sequence 110 AA;

Query Match 91.6%; Score 537; DB 8; Length 110;

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  Best Local Similarity   94.5%;  Pred. No. 4.6e-37;
  Matches  104;  Conservative    1;  Mismatches    5;  Indels    0;  Gaps    0;

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Db          1 QSVLTQPPSVSAAPGQKVTISCSGSSSNIGNNYVSWYQQLPGTAPKLLIYDNNKRPSGIP 60

Qy         61 DRFSGSKSGTSATLGITGLQTGDEADYYCXTWDSSLSAVVFGGGTKLTVL 110
              |||||||||||||||||||||||||||| |||||||| ||||||||||
Db         61 DRFSGSKSGTSATLGITGLQTGDEADYYCGTWDSSLSAGVFGGGTKLTVL 110


RESULT 13
ADP22403
ID   ADP22403 standard; protein; 110 AA.
XX
AC   ADP22403;
XX
DT   09-SEP-2004  (first entry)
XX
DE   Human anti-TNFa antibody light chain variable region SEQ ID NO:309.
XX
KW   human; monoclonal antibody; tumour necrosis factor-alpha; TNFa;
KW   anti-TNFa antibody; anabolic; antiarteriosclerotic; antiarthritic;
KW   antibacterial; antiinflammatory; antipsoriatic; antirheumatic;
KW   eating-disorder; immunomodulator; immunosuppressive; nephrotropic;
KW   neuroprotective; vasotropic; antiapoptotic; TNFa antagonist;
KW   TNF induced apoptosis; neoplastic disease; breast cancer; ovarian cancer;
KW   bladder cancer; lung cancer; glioblastoma; stomach cancer;
KW   endometrial cancer; kidney cancer; colon cancer; pancreatic cancer;
KW   prostrate cancer; immuno-mediated inflammatory disease;
KW   rheumatoid arthritis; glomerulonephritis; atherosclerosis; psoriasis;
KW   restenosis; autoimmune disease; Crohn's disease; graft-host reaction;
KW   septic shock; cachexia; anorexia; multiple sclerosis.
XX
OS   Homo sapiens.
XX
PN   WO2004050683-A2.
XX
PD   17-JUN-2004.
XX
PF   02-DEC-2003; 2003WO-US038281.
XX
PR   02-DEC-2002; 2002US-0430729P.
XX
PA   (ABGE-) ABGENIX INC.
XX
PI   Babcook JS,  Kang JS,  Foord O,  Green L,  Feng X,  Klakamp S;
PI   Haak-Frendscho M,  Rathanaswami P,  Pigott C,  Liang ML,  Lee R;
PI   Manchulencho K,  Faggioni R,  Senaldi G,  Qiaojuan JS;
XX
DR   WPI; 2004-480601/45.
XX
PT   New recombinant human monoclonal antibody that specifically binds to
PT   Tumor Necrosis Factor-alpha, useful for treating neoplastic disease such
PT   as cancers, or immuno-mediated inflammatory diseases such as rheumatoid
PT   arthritis.
XX
PS   Example 10; SEQ ID NO 309; 213pp; English.
XX
CC   The present invention describes a human monoclonal antibody (I) that
CC   specifically binds to tumour necrosis factor-alpha (TNFa) and comprises:
CC   (a) a heavy chain complementarity determining region 1 (CDR1) having the
CC   two fully defined 5 amino acid sequence (S1, ADP22417) or (S2, ADP22421);
CC   and (b) a light chain CDR1 having the two fully defined 11 amino acid
CC   sequence (S3, ADP22418) or (S4, ADP22424). Also described: (1) assaying
CC   (M1) the level of TNFa in a patient sample, comprising contacting with
CC   (I), and detecting the level of binding between the antibody and TNFa in
CC   the sample; (2) a composition comprising the antibody or its functional
CC   fragment and a carrier; (3) treating (M2) an animal suffering from a
CC   neoplastic, or an immuno-mediated inflammatory disease by selecting an
CC   animal in need of treatment for the disease by administering the human
CC   monoclonal antibody of (I); and (4) inhibiting (M3) TNFa induced
CC   apoptosis in an animal by selecting an animal in need of treatment for
CC   TNFa induced apoptosis by administering the human monoclonal antibody of
CC   (I). (I) has anabolic, antiarteriosclerotic, antiarthritic,
CC   antibacterial, antiinflammatory, antipsoriatic, antirheumatic, eating-
CC   disorders, immunomodulator, immunosuppressive, nephrotropic,
CC   neuroprotective, vasotropic and antiapoptotic activities, and can be used
CC   as a TNFa antagonist. The antibody (I) is useful in the preparation of
CC   medicament for treating TNF induced apoptosis, neoplastic disease such as
CC   breast cancer, ovarian cancer, bladder cancer, lung cancer, glioblastoma,
CC   stomach cancer, endometrial cancer, kidney cancer, colon cancer,
CC   pancreatic cancer, and prostrate cancer; or immuno-mediated inflammatory
CC   diseases such as rheumatoid arthritis, glomerulonephritis,
CC   atherosclerosis, psoriasis, restenosis, autoimmune disease, Crohn's
CC   disease, graft-host reactions, septic shock, cachexia, anorexia, and
CC   multiple sclerosis. The present sequence represents a human anti-TNFa
CC   antibody light chain variable region, which is used in the
CC   exemplification of the present invention.
XX
SQ   Sequence 110 AA;

  Query Match             91.6%;  Score 537;  DB 8;  Length 110;
  Best Local Similarity   94.5%;  Pred. No. 4.6e-37;
  Matches  104;  Conservative    1;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 QSVLTQPPSVSAAPGQKVTISCSGSSSNIGNNFVSWYQQLPGTAPXLLIYDITKRPSGIP 60
              ||||||||||||||||||||||||||||||:||||||||||| |||||  |||||||
Db          1 QSVLTQPPSVSAAPGQKVTISCSGSSSNIGNNYVSWYQQLPGTAPKLLIYDNNKRPSGIP 60

Qy         61 DRFSGSKSGTSATLGITGLQTGDEADYYCXTWDSSLSAVVFGGGTKLTVL 110
              |||||||||||||||||||||||||||| |||||||| ||||||||||
Db         61 DRFSGSKSGTSATLGITGLQTGDEADYYCGTWDSSLSAGVFGGGTKLTVL 110


RESULT 14
ABP45249
ID   ABP45249 standard; protein; 258 AA.
XX
AC   ABP45249;
XX
DT   19-AUG-2002  (first entry)
XX
DE   Human BLyS binding scFv SEQ ID 1260.
XX
KW   BLys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
KW   tumour necrosis factor; B cell proliferation; B cell differentiation;
KW   immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;
KW   antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
KW   systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
KW   common variable immunodeficiency; acquired immunodeficiency syndrome.
XX
OS   Homo sapiens.
XX
PN   WO200202641-A1.
XX
PD   10-JAN-2002.
XX
PF   15-JUN-2001; 2001WO-US019110.
XX
PR   16-JUN-2000; 2000US-0212210P.
PR   17-OCT-2000; 2000US-0240816P.
PR   16-MAR-2001; 2001US-0276248P.
PR   21-MAR-2001; 2001US-0277379P.
PR   25-MAY-2001; 2001US-0293499P.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
PA   (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX
PI   Ruben SM,  Barash SC,  Choi GH,  Vaughan T,  Hilbert D;
XX
DR   WPI; 2002-114799/15.
XX
PT   Antibodies against B Lymphocyte Stimulating polypeptides, useful for the
PT   diagnosis and treatment of cancers and immune disorders.
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```
XX
PS   Claim 1; Page 1906-1907; 3148pp; English.
XX
CC   This invention describes novel antibodies that immunospecifically bind to
CC   B Lymphocyte Stimulator (BLyS) polypeptides. BLyS is a member of the
CC   tumour necrosis factor (TNF) super family and induces B cell
CC   proliferation and differentiation. The antibodies of the invention have
CC   cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
CC   antirheumatic and antiAIDS activity and can be used in vaccines to
CC   inhibit the expression and activity of BLyS. The antibodies bind to BLyS
CC   and so may be used to detect and quantitate the presence of BLyS in
CC   biological samples and may be used in this way to diagnose disease
CC   associated with aberrant expression of BLyS. They may also be
CC   administered to treat diseases associated with aberrant BLyS expression
CC   and activity such as cancer, immune, and autoimmune disorders and
CC   diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
CC   immunodeficiency (e.g. common variable immunodeficiency (CVID) and
CC   acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
CC   the antibodies and fragments of the antibodies described in the method of
CC   the invention
XX
SQ   Sequence 258 AA;

  Query Match             91.1%;  Score 534;  DB 5;  Length 258;
  Best Local Similarity   92.8%;  Pred. No. 1.9e-36;
  Matches  103;  Conservative    1;  Mismatches    7;  Indels    0;  Gaps    0;

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              ||||||||||||||||||||||||||||||:||||||||||| |||||  |||||||
Db        148 QSVLTQPPSVSAAPGQKVTISCSGSSSNIGNNYVSWYQQLPGTAPKLLIYDNNKRPSGIP 207

Qy         61 DRFSGSKSGTSATLGITGLQTGDEADYYCXTWDSSLSAVVFGGGTKLTVLG 111
              |||||||||||||||||||||||||||||  ||||||| ||| ||||||||
Db        208 DRFSGSKSGTSATLGITGLQTGDEADYYCGAWDSSLSAYVFGSGTKLTVLG 258


RESULT 15
ADG96076
ID   ADG96076 standard; protein; 258 AA.
XX
AC   ADG96076;
XX
DT   11-MAR-2004  (first entry)
XX
DE   Single chain antibody that immunospecifically binds BLyS SeqID 1260.
XX
KW   antibody; B lymphocyte stimulator; BLyS; tumour necrosis factor;
KW   B cell proliferation; differentiation; scFv; myasthenia gravis;
KW   multiple sclerosis; asthma; rheumatoid arthritis; AIDS; leukaemia;
KW   carcinoma; lymphoma; antirheumatic; antiarthritic; neuroprotective;
KW   antiinflammatory; antiasthmatic; antiallergic; cytostatic.
XX
OS   Unidentified.
XX
PN   WO2003055979-A2.
XX
PD   10-JUL-2003.
XX
PF   14-NOV-2002; 2002WO-US036496.
XX
PR   16-NOV-2001; 2001US-0331469P.
PR   19-DEC-2001; 2001US-0340817P.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
XX
PI   Ruben SM,  Barash SC,  Choi GH,  Vaughan TJ,  Hilbert D;
XX
DR   WPI; 2003-505530/47.
XX
PT   Novel antibody that immunospecifically binds to a B lymphocyte stimulator
PT   (BLys), useful for detecting and treating diseases or disorders e.g.
PT   rheumatoid arthritis, asthma and leukemia.
XX
PS   Example 1; SEQ ID NO 1260; 394pp; English.
XX
CC   This invention relates to novel antibodies that immunospecifically bind
CC   to B lymphocyte stimulator (BLyS). The BLyS gene has been mapped to
CC   chromosome 13q34 and encodes a protein that is a member of the tumour
CC   necrosis factor superfamily and induces both in vivo and in vitro B cell
CC   proliferation and differentiation. Specifically, it refers to single
CC   chain antibody molecules (scFvs) derived, preferably, from the variable
CC   heavy CDR3 region that immunospecifically bind to a polypeptide, or
CC   fragment thereof, of either human, murine, rat or monkey BLyS. The
CC   present invention refers to the use of such antibodies in various methods
CC   for the detection, diagnosis and prognosis of diseases related to the
CC   aberrant expression or inappropriate function of BLyS or its receptor. As
CC   such, these compositions are useful for identifying immune disorders
CC   including myasthenia gravis and multiple sclerosis, inflammatory
CC   disorders e.g. asthma and rheumatoid arthritis, infectious diseases such
CC   as AIDS and proliferative disorders including leukaemia, carcinoma and
CC   lymphoma. Accordingly, they can be described as exhibiting various
CC   activities such as antirheumatic, antiarthritic, neuroprotective,
CC   antiinflammatory, antiasthmatic, antiallergic and cytostatic. This
CC   polypeptide sequence is a single chain antibody that binds BLyS of the
CC   invention. NOTE: The sequence data for this patent did not form part of
CC   the printed specification, but was obtained in electronic format
CC   directely from WIPO at ftp.wipo.int/pub/published pct_sequences.
XX
SQ   Sequence 258 AA;

  Query Match             91.1%;  Score 534;  DB 7;  Length 258;
  Best Local Similarity   92.8%;  Pred. No. 1.9e-36;
  Matches  103;  Conservative    1;  Mismatches    7;  Indels    0;  Gaps    0;

Qy          1 QSVLTQPPSVSAAPGQKVTISCSGSSSNIGNNFVSWYQQLPGTAPXLLIYDITKRPSGIP 60
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Db        148 QSVLTQPPSVSAAPGQKVTISCSGSSSNIGNNYVSWYQQLPGTAPKLLIYDNNKRPSGIP 207

Qy         61 DRFSGSKSGTSATLGITGLQTGDEADYYCXTWDSSLSAVVFGGGTKLTVLG 111
              |||||||||||||||||||||||||||||  ||||||| ||| ||||||||
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Search completed: October 13, 2005, 03:06:57
Job time : 119.425 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

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Title: US-10-010-729A-7
Perfect score: 615
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Scoring table: BLOSUM62
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Searched: 1854112 seqs, 416015017 residues

Total number of hits satisfying chosen parameters: 1854112

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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21: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
22: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	611	99.3	119	14	US-10-010-729-7	Sequence 7, Appli
2	544	88.5	123	14	US-10-269-805-21	Sequence 21, Appl
3	542.5	88.2	248	14	US-10-235-175-80	Sequence 80, Appl
4	540.5	87.9	120	15	US-10-371-942-18	Sequence 18, Appl
5	540.5	87.9	121	17	US-10-726-332-23	Sequence 23, Appl
6	540	87.8	121	17	US-10-727-155-190	Sequence 190, App
7	540	87.8	123	15	US-10-292-088-115	Sequence 115, App
8	539	87.6	119	14	US-10-120-377-76	Sequence 76, Appl
9	539	87.6	119	17	US-10-980-815-76	Sequence 76, Appl
10	539	87.6	119	18	US-10-992-196-76	Sequence 76, Appl
11	538.5	87.6	241	17	US-10-935-290-100	Sequence 100, App
12	538	87.5	113	10	US-09-791-153A-63	Sequence 63, Appl
13	537	87.3	117	20	US-11-021-715-57	Sequence 57, Appl
14	537	87.3	121	17	US-10-727-155-92	Sequence 92, Appl
15	535.5	87.1	117	17	US-10-938-353-110	Sequence 110, App
16	535	87.0	117	20	US-11-021-715-59	Sequence 59, Appl
17	535	87.0	244	17	US-10-935-290-55	Sequence 55, Appl
18	535	87.0	519	16	US-10-312-354-19	Sequence 19, Appl
19	534.5	86.9	118	14	US-10-120-377-78	Sequence 78, Appl
20	534.5	86.9	118	17	US-10-980-815-78	Sequence 78, Appl
21	534.5	86.9	118	18	US-10-992-196-78	Sequence 78, Appl
22	534	86.8	117	20	US-11-021-715-58	Sequence 58, Appl
23	533	86.7	115	20	US-11-047-996-89	Sequence 89, Appl
24	532.5	86.6	121	17	US-10-726-332-142	Sequence 142, App
25	532	86.5	127	17	US-10-706-689-36	Sequence 36, Appl
26	532	86.5	127	18	US-10-988-360-36	Sequence 36, Appl
27	532	86.5	463	17	US-10-938-353-18	Sequence 18, Appl
28	531.5	86.4	116	15	US-10-309-764-3	Sequence 3, Appli
29	531.5	86.4	135	15	US-10-309-764-59	Sequence 59, Appl
30	530.5	86.3	126	15	US-10-309-762-133	Sequence 133, App
31	530.5	86.3	252	10	US-09-880-748-1627	Sequence 1627, Ap
32	530.5	86.3	252	15	US-10-293-418-1627	Sequence 1627, Ap
33	530	86.2	124	17	US-10-725-962-12	Sequence 12, Appl
34	529.5	86.1	121	17	US-10-726-332-136	Sequence 136, App
35	529.5	86.1	252	10	US-09-880-748-1519	Sequence 1519, Ap
36	529.5	86.1	252	15	US-10-293-418-1519	Sequence 1519, Ap
37	529	86.0	115	17	US-10-884-830-35	Sequence 35, Appl
38	529	86.0	124	17	US-10-805-177-54	Sequence 54, Appl
39	528.5	85.9	249	10	US-09-880-748-512	Sequence 512, App
40	528.5	85.9	249	15	US-10-293-418-512	Sequence 512, App
41	528	85.9	117	17	US-10-638-265-18	Sequence 18, Appl
42	528	85.9	125	15	US-10-292-088-107	Sequence 107, App
43	527.5	85.8	116	15	US-10-309-764-9	Sequence 9, Appli
44	527.5	85.8	116	15	US-10-309-764-10	Sequence 10, Appl
45	527.5	85.8	135	15	US-10-309-764-71	Sequence 71, Appl

ALIGNMENTS

RESULT 1
US-10-010-729-7
; Sequence 7, Application US/10010729
; Publication No. US20030185827A1
; GENERAL INFORMATION:
; APPLICANT: Rodriguez, Moses
; APPLICANT: Miller, David J.
; APPLICANT: Pease, Larry R.
; TITLE OF INVENTION: Human IgM Antibodies and Diagnostic and
; TITLE OF INVENTION: Therapeutic Uses Thereof Particularly in the Central Nervous
; TITLE OF INVENTION: System
; FILE REFERENCE: 1199-1-005CIP2
; CURRENT APPLICATION NUMBER: US/10/010,729
; CURRENT FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: 09/730,473
; PRIOR FILING DATE: 2000-12-05
; PRIOR APPLICATION NUMBER: 09/580,787
; PRIOR FILING DATE: 2000-05-30
; PRIOR APPLICATION NUMBER: 09/322,862
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 08/779,784
; PRIOR FILING DATE: 1997-01-07
; PRIOR APPLICATION NUMBER: 08/692,084
; PRIOR FILING DATE: 1996-08-08
; PRIOR APPLICATION NUMBER: 08/236,520
; PRIOR FILING DATE: 1994-04-29
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-010-729-7

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  Query Match             99.3%;  Score 611;  DB 14;  Length 119;
  Best Local Similarity   98.3%;  Pred. No. 9.6e-50;
  Matches  117;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

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RESULT 2
US-10-269-805-21
; Sequence 21, Application US/10269805
; Publication No. US20030124129A1
; GENERAL INFORMATION:
;  APPLICANT: OLINER, JONATHAN D.
;  TITLE OF INVENTION: ANGIOPOIETIN-2 SPECIFIC BINDING AGENTS
;  FILE REFERENCE: A-722
;  CURRENT APPLICATION NUMBER: US/10/269,805
;  CURRENT FILING DATE:  2002-10-10
;  PRIOR APPLICATION NUMBER: US 60/328,604
;  PRIOR FILING DATE: 2001-10-11
;  NUMBER OF SEQ ID NOS: 76
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 21
;   LENGTH: 123
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-269-805-21

  Query Match             88.5%;  Score 544;  DB 14;  Length 123;
  Best Local Similarity   87.0%;  Pred. No. 2e-43;
  Matches  107;  Conservative    1;  Mismatches   11;  Indels    4;  Gaps    1;

Qy          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSSGMHWVRQAPGKGLEWVAXISYDGSRKYY 60
              |||| |||||||||||||||||||||||| |||||||||||||||| |||||| |||
Db          1 QVQLQESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVISYDGSNKYY 60

Qy         61 ADSVKGRFTISRDNSKNTLYLQMNSLTAXDTAVYYCAKGVT----GSPTLDYWGQGTLVT 116
              ||||||||||||||||||||||||| | |||||||||      |   :|||||||||
Db         61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKGPVDFDYGDYAIDYWGQGTLVT 120

Qy        117 VSS 119
              |||
Db        121 VSS 123


RESULT 3
US-10-235-175-80
; Sequence 80, Application US/10235175
; Publication No. US20030166287A1
; GENERAL INFORMATION:
;  APPLICANT: Es van, Helmuth
;  APPLICANT:  Havenga, Menzo
;  APPLICANT:  Verlinden, Stefan
;  TITLE OF INVENTION: TARGETED DELIVERY THROUGH A CATIONIC AMINO ACID
;  TITLE OF INVENTION:  TRANSPORTER
;  FILE REFERENCE: 2183-4080US
;  CURRENT APPLICATION NUMBER: US/10/235,175
;  CURRENT FILING DATE:  2002-09-04
;  PRIOR APPLICATION NUMBER: US/09/315,926
;  PRIOR FILING DATE: 1999-05-20
;  PRIOR APPLICATION NUMBER: EP 99201593.3
;  PRIOR FILING DATE: 1999-05-20
;  PRIOR APPLICATION NUMBER: EP 98201693.3
;  PRIOR FILING DATE: 1998-05-20
;  NUMBER OF SEQ ID NOS: 81
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 80
;   LENGTH: 248
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: Description of Artificial Sequence: phage
;   FEATURE:
;   NAME/KEY: PEPTIDE
;   LOCATION: (1)..(248)
;   OTHER INFORMATION: /note="hCAT1 amino acid sequence"
US-10-235-175-80

  Query Match             88.2%;  Score 542.5;  DB 14;  Length 248;
  Best Local Similarity   87.5%;  Pred. No. 5.6e-43;
  Matches  105;  Conservative    5;  Mismatches    9;  Indels    1;  Gaps    1;

Qy          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSSGMHWVRQAPGKGLEWVAXISYDGSRKYY 60
              |||||:|||||||||||||||||||||||  |||||||||||||| |||||| |||
Db         23 QVQLVQSGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYY 82

Qy         61 ADSVKGRFTISRDNSKNTLYLQMNSLTAXDTAVYYCAKGVTGSPT-LDYWGQGTLVTVSS 119
              |||||||||||||||||||||||||| | ||||||||:|:| : :  ||||||||||||
Db         83 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARGITVTKSRFDYWGQGTLVTVSS 142


RESULT 4
US-10-371-942-18
; Sequence 18, Application US/10371942
; Publication No. US20030223994A1
; GENERAL INFORMATION:
;  APPLICANT: Hoogenboom, Henricus Renerus Jacobus Mattheus
;  APPLICANT:  Reiter, Yoram
;  TITLE OF INVENTION: MHC-PEPTIDE COMPLEX BINDING LIGANDS
;  FILE REFERENCE: 10280-034001
;  CURRENT APPLICATION NUMBER: US/10/371,942
;  CURRENT FILING DATE:  2003-02-20
;  PRIOR APPLICATION NUMBER: US 60/358,994
;  PRIOR FILING DATE: 2002-02-20
;  NUMBER OF SEQ ID NOS: 121
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 18
;   LENGTH: 120
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-371-942-18

  Query Match             87.9%;  Score 540.5;  DB 15;  Length 120;
  Best Local Similarity   88.3%;  Pred. No. 4.1e-43;
  Matches  106;  Conservative    2;  Mismatches   11;  Indels    1;  Gaps    1;

Qy          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSSGMHWVRQAPGKGLEWVAXISYDGSRKYY 60
              |||||:|||||||||||||||||||||||| |||||||||||||||| |||||| |||
Db          1 QVQLVQSGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVISYDGSNKYY 60

Qy         61 ADSVKGRFTISRDNSKNTLYLQMNSLTAXDTAVYYCAKGVTGS-PTLDYWGQGTLVTVSS 119
              |||||||||||||||||||||||||| | ||||||||:   |    ||||||||||||||
Db         61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDYYGDYALLDYWGQGTLVTVSS 120


RESULT 5
US-10-726-332-23
; Sequence 23, Application US/10726332
; Publication No. US20050058649A1
; GENERAL INFORMATION:
;  APPLICANT: Gregory M. Landes
;  APPLICANT:  Mary Haak-Frendscho
;  APPLICANT:  Ling Chen
;  APPLICANT:  Yen-Wah R. Lee
;  APPLICANT:  Meina Liang
;  APPLICANT:  Xiao Feng
;  APPLICANT:  Xiao-Chi Jia
;  APPLICANT:  Mark R. Nocerini
;  TITLE OF INVENTION: ANTIBODIES DIRECTED TO PHOSPHOLIPASE A2
;  TITLE OF INVENTION:  AND USES THEREOF
```

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;  FILE REFERENCE: ABGENIX.072A
;  CURRENT APPLICATION NUMBER: US/10/726,332
;  CURRENT FILING DATE:  2003-12-02
;  PRIOR APPLICATION NUMBER: n/a
;  PRIOR FILING DATE:
;  NUMBER OF SEQ ID NOS: 222
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 23
;   LENGTH: 121
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-726-332-23

  Query Match             87.9%;  Score 540.5;  DB 17;  Length 121;
  Best Local Similarity   87.5%;  Pred. No. 4.1e-43;
  Matches  105;  Conservative    4;  Mismatches   10;  Indels    1;  Gaps    1;

Qy          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSSGMHWVRQAPGKGLEWVAXISYDGSRKYY 60
              |||||||||||||||||||||||||||||| |||||||||||||||| | |||| |:|
Db          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAAIWYDGSNKWY 60

Qy         61 ADSVKGRFTISRDNSKNTLYLQMNSLTAXDTAVYYCAKGVTGSP-TLDYWGQGTLVTVSS 119
              |||||||||||||||||||||||| | ||||||||:| ||:|   | |||||:|||||
Db         61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARGGTGTPGAPDIWGQGTMVTVSS 120


RESULT 6
US-10-727-155-190
; Sequence 190, Application US/10727155
; Publication No. US20050049402A1
; GENERAL INFORMATION:
;  APPLICANT: John S. Babcook
;  APPLICANT:  Jaspal S. Kang
;  APPLICANT:  Orit Foord
;  APPLICANT:  Larry Green
;  APPLICANT:  Xiao Feng
;  APPLICANT:  Scott Klakamp
;  APPLICANT:  Mary Haak-Frendscho
;  APPLICANT:  Palaniswami Rathanaswami
;  APPLICANT:  Craig Pigott
;  APPLICANT:  Meina Liang
;  APPLICANT:  Rozanne Lee
;  APPLICANT:  Kathy Manchulencho
;  APPLICANT:  Raffaella Faggioni
;  APPLICANT:  Giorgio Senaldi
;  APPLICANT:  Qiaojuan Jane Su
;  TITLE OF INVENTION: ANTIBODIES DIRECTED TO TUMOR NECROSIS
;  TITLE OF INVENTION:  FACTOR AND USES THEREOF
;  FILE REFERENCE: ABGENIX.073A
;  CURRENT APPLICATION NUMBER: US/10/727,155
;  CURRENT FILING DATE:  2003-12-02
;  PRIOR APPLICATION NUMBER: 60/430729
;  PRIOR FILING DATE: 2002-12-02
;  NUMBER OF SEQ ID NOS: 320
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 190
;   LENGTH: 121
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-727-155-190

  Query Match             87.8%;  Score 540;  DB 17;  Length 121;
  Best Local Similarity   87.6%;  Pred. No. 4.6e-43;
  Matches  106;  Conservative    2;  Mismatches   11;  Indels    2;  Gaps    1;

Qy          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSSGMHWVRQAPGKGLEWVAXISYDGSRKYY 60
              |||||||||||||||||||||||||||||| |||||||||||||||| | |||| |||
Db          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVIWYDGSNKYY 60

Qy         61 ADSVKGRFTISRDNSKNTLYLQMNSLTAXDTAVYYCAK--GVTGSPTLDYWGQGTLVTVS 118
              |||||||||||||||||||||||| | ||||||||:     |:|  ||||||||||||
Db         61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAREGDYGGNPYFDYWGQGTLVTVS 120

Qy        119 S 119
              |
Db        121 S 121


RESULT 7
US-10-292-088-115
; Sequence 115, Application US/10292088
; Publication No. US20030211100A1
; GENERAL INFORMATION:
;  APPLICANT: BEDIAN, VAHE
;  APPLICANT:  GLADUE, RONALD P.
;  APPLICANT:  CORVALAN, JOSE
;  APPLICANT:  JIA, XIAO-CHI
;  APPLICANT:  FENG, XIAO
;  TITLE OF INVENTION: ANTIBODIES TO CD40
;  FILE REFERENCE: ABX-PF/3 US
;  CURRENT APPLICATION NUMBER: US/10/292,088
;  CURRENT FILING DATE:  2003-03-14
;  PRIOR APPLICATION NUMBER: 60/348,980
;  PRIOR FILING DATE: 2001-11-09
;  NUMBER OF SEQ ID NOS: 147
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 115
;   LENGTH: 123
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-292-088-115

  Query Match             87.8%;  Score 540;  DB 15;  Length 123;
  Best Local Similarity   86.2%;  Pred. No. 4.7e-43;
  Matches  106;  Conservative    3;  Mismatches   10;  Indels    4;  Gaps    1;

Qy          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSSGMHWVRQAPGKGLEWVAXISYDGSRKYY 60
              |||||||||||||||||||||||||||||| |||||||||||||||| |||||| |||
Db          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVISYDGSNKYY 60

Qy         61 ADSVKGRFTISRDNSKNTLYLQMNSLTAXDTAVYYCAKGVTGS----PTLDYWGQGTLVT 116
              |||||||||||||||||||||||| | ||||||||:| ||:      :| ||||| ||
Db         61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARGTTGTYYYYYGMDVWGQGTTVT 120

Qy        117 VSS 119
              |||
Db        121 VSS 123


RESULT 8
US-10-120-377-76
; Sequence 76, Application US/10120377
; Publication No. US20030176674A1
; GENERAL INFORMATION:
;  APPLICANT: Rosen, Craig, et al.
;  TITLE OF INVENTION: Vascular Endothelial Growth Factor-2
;  FILE REFERENCE: PF112P8
;  CURRENT APPLICATION NUMBER: US/10/120,377
;  CURRENT FILING DATE:  2002-04-12
;  PRIOR APPLICATION NUMBER: 60/283,391
;  PRIOR FILING DATE: 2001-04-13
;  PRIOR APPLICATION NUMBER: 60/317,600
;  PRIOR FILING DATE: 2001-09-07
;  NUMBER OF SEQ ID NOS: 79
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 76
;   LENGTH: 119
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-120-377-76

  Query Match             87.6%;  Score 539;  DB 14;  Length 119;
  Best Local Similarity   88.2%;  Pred. No. 5.6e-43;
  Matches  105;  Conservative    1;  Mismatches   13;  Indels    0;  Gaps    0;

Qy          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSSGMHWVRQAPGKGLEWVAXISYDGSRKYY 60
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```
Db          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSRYGMHWVRQAPGKGLEWVALIWYDGSNKYY 60

Qy         61 ADSVKGRFTISRDNSKNTLYLQMNSLTAXDTAVYYCAKGVTGSPTLDYWGQGTLVTVSS 119
              ||||||||||||||||||||||||| | ||||||||: ||  ||||||||||||
Db         61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDGFGSGCFDYWGQGTLVTVSS 119


RESULT 9
US-10-980-815-76
; Sequence 76, Application US/10980815
; Publication No. US20050059117A1
; GENERAL INFORMATION:
;  APPLICANT: Rosen, Craig, et al.
;  TITLE OF INVENTION: Vascular Endothelial Growth Factor-2
;  FILE REFERENCE: PF112P8
;  CURRENT APPLICATION NUMBER: US/10/980,815
;  CURRENT FILING DATE:  2004-11-04
;  PRIOR APPLICATION NUMBER: US/10/120,377
;  PRIOR FILING DATE: 2002-04-12
;  PRIOR APPLICATION NUMBER: 60/283,391
;  PRIOR FILING DATE: 2001-04-13
;  PRIOR APPLICATION NUMBER: 60/317,600
;  PRIOR FILING DATE: 2001-09-07
;  NUMBER OF SEQ ID NOS: 79
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 76
;   LENGTH: 119
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-980-815-76

  Query Match           87.6%;  Score 539;  DB 17;  Length 119;
  Best Local Similarity  88.2%;  Pred. No. 5.6e-43;
  Matches  105;  Conservative    1;  Mismatches   13;  Indels    0;  Gaps    0;

Qy          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSSGMHWVRQAPGKGLEWVAXISYDGSRKYY 60
              ||||||||||||||||||||||||||  |||||||||||||||| | |||| |||
Db          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSRYGMHWVRQAPGKGLEWVALIWYDGSNKYY 60

Qy         61 ADSVKGRFTISRDNSKNTLYLQMNSLTAXDTAVYYCAKGVTGSPTLDYWGQGTLVTVSS 119
              ||||||||||||||||||||||||| | ||||||||:  ||  ||||||||||||
Db         61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDGFGSGCFDYWGQGTLVTVSS 119


RESULT 10
US-10-992-196-76
; Sequence 76, Application US/10992196
; Publication No. US20050192429A1
; GENERAL INFORMATION:
;  APPLICANT: Rosen, Craig, et al.
;  TITLE OF INVENTION: Vascular Endothelial Growth Factor-2
;  FILE REFERENCE: PF112P8P1
;  CURRENT APPLICATION NUMBER: US/10/992,196
;  CURRENT FILING DATE:  2004-11-19
;  PRIOR APPLICATION NUMBER: 60/523,661
;  PRIOR FILING DATE: 2003-11-21
;  PRIOR APPLICATION NUMBER: 60/283,391
;  PRIOR FILING DATE: 2001-04-13
;  PRIOR APPLICATION NUMBER: 60/317,600
;  PRIOR FILING DATE: 2001-09-07
;  PRIOR APPLICATION NUMBER: 10/120,377
;  PRIOR FILING DATE: 2002-04-12
;  NUMBER OF SEQ ID NOS: 83
; SEQ ID NO 76
;   LENGTH: 119
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-992-196-76

  Query Match           87.6%;  Score 539;  DB 18;  Length 119;
  Best Local Similarity  88.2%;  Pred. No. 5.6e-43;
  Matches  105;  Conservative    1;  Mismatches   13;  Indels    0;  Gaps    0;

Qy          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSSGMHWVRQAPGKGLEWVAXISYDGSRKYY 60
              ||||||||||||||||||||||||||  |||||||||||||||| | |||| |||
Db          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSRYGMHWVRQAPGKGLEWVALIWYDGSNKYY 60

Qy         61 ADSVKGRFTISRDNSKNTLYLQMNSLTAXDTAVYYCAKGVTGSPTLDYWGQGTLVTVSS 119
              ||||||||||||||||||||||||| | ||||||||:  ||  ||||||||||||
Db         61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDGFGSGCFDYWGQGTLVTVSS 119


RESULT 11
US-10-935-290-100
; Sequence 100, Application US/10935290
; Publication No. US20050069542A1
; GENERAL INFORMATION:
;  APPLICANT: Baker et al.
;  TITLE OF INVENTION: Antibodies that Specifically Bind to GMAD
;  FILE REFERENCE: PF584P1
;  CURRENT APPLICATION NUMBER: US/10/935,290
;  CURRENT FILING DATE:  2004-09-08
;  PRIOR APPLICATION NUMBER: PCT/US03/09625
;  PRIOR FILING DATE: 2003-03-28
;  PRIOR APPLICATION NUMBER: 60/368,813
;  PRIOR FILING DATE: 2002-04-01
;  NUMBER OF SEQ ID NOS: 234
; SEQ ID NO 100
;   LENGTH: 241
;   TYPE: PRT
;   ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: scFv protein GMBC683
US-10-935-290-100

  Query Match           87.6%;  Score 538.5;  DB 17;  Length 241;
  Best Local Similarity  88.2%;  Pred. No. 1.3e-42;
  Matches  105;  Conservative    2;  Mismatches   11;  Indels    1;  Gaps    1;

Qy          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSSGMHWVRQAPGKGLEWVAXISYDGSRKYY 60
              :|||||||||:|||||||||||||||||||| |||||||||||||||| |||||| |||
Db          1 EVQLVESGGGLVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVISYDGSNKYY 60

Qy         61 ADSVKGRFTISRDNSKNTLYLQMNSLTAXDTAVYYCAKGVTGSPTLDYWGQGTLVTVSS 119
              |||||||||||||||||||||||| | |||||||||      |||||||| |||||
Db         61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKRAAAG-TLDYWGQGTTVTVSS 118


RESULT 12
US-09-791-153A-63
; Sequence 63, Application US/09791153A
; Publication No. US20030103978A1
; GENERAL INFORMATION:
;  APPLICANT: Deshpande, Rajendra
;  APPLICANT:  Hitz, Anna
;  APPLICANT:  Boyle, William
;  APPLICANT:  Sullivan, John
;  TITLE OF INVENTION: SELECTIVE BINDING AGENTS OF OSTEOPROTEGERIN BINDING PROTEIN
;  FILE REFERENCE: A-633A
;  CURRENT APPLICATION NUMBER: US/09/791,153A
;  CURRENT FILING DATE:  2001-07-17
;  PRIOR APPLICATION NUMBER: 09/511,139
;  PRIOR FILING DATE: 2000-02-23
;  NUMBER OF SEQ ID NOS: 154
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 63
;   LENGTH: 113
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-791-153A-63

  Query Match           87.5%;  Score 538;  DB 10;  Length 113;
  Best Local Similarity  89.1%;  Pred. No. 6.6e-43;
  Matches  106;  Conservative    0;  Mismatches    7;  Indels    6;  Gaps    1;
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```
Qy          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSSGMHWVRQAPGKGLEWVAXISYDGSRKYY 60
              |||||||||||||||||||||||||||||||| |||||||||||||||| |||||| |||
Db          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVISYDGSNKYY 60

Qy         61 ADSVKGRFTISRDNSKNTLYLQMNSLTAXDTAVYYCAKGVTGSPTLDYWGQGTLVTVSS 119
              |||||||||||||||||||||||| | |||||||||       ||||||||||||||
Db         61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAK------YFDYWGQGTLVTVSS 113


RESULT 13
US-11-021-715-57
; Sequence 57, Application US/11021715
; Publication No. US20050208596A1
; GENERAL INFORMATION:
;  APPLICANT: Siegel, Donald L.
;  TITLE OF INVENTION: COMPOSITIONS, METHODS AND KITS RELATING TO ANTI-PLATELET
;  TITLE OF INVENTION:  AUTOANTIBODIES AND INHIBITORS THEREOF
;  FILE REFERENCE: 053893-5050
;  CURRENT APPLICATION NUMBER: US/11/021,715
;  CURRENT FILING DATE:  2004-12-23
;  PRIOR APPLICATION NUMBER: PCT/US03/21304
;  PRIOR FILING DATE: 2003-07-03
;  PRIOR APPLICATION NUMBER: 60/394,352
;  PRIOR FILING DATE: 2002-07-03
;  PRIOR APPLICATION NUMBER: 60/411,694
;  PRIOR FILING DATE: 2002-09-18
;  NUMBER OF SEQ ID NOS: 153
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 57
;   LENGTH: 117
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-021-715-57

  Query Match             87.3%;  Score 537;  DB 20;  Length 117;
  Best Local Similarity   88.2%;  Pred. No. 8.5e-43;
  Matches  105;  Conservative    1;  Mismatches   11;  Indels    2;  Gaps    1;

Qy          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSSGMHWVRQAPGKGLEWVAXISYDGSRKYY 60
              |||||||||||||||||||||||||||||||  |||||||||||||||| |||||| |||
Db          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYY 60

Qy         61 ADSVKGRFTISRDNSKNTLYLQMNSLTAXDTAVYYCAKGVTGSPTLDYWGQGTLVTVSS 119
              |||||||||||||||||||||||||   ||||||||:|  |    |||||||||||||
Db         61 ADSVKGRFTISRDNSKNTLYLQMNSLRPEDTAVYYCARG--GVAAFDYWGQGTLVTVSS 117


RESULT 14
US-10-727-155-92
; Sequence 92, Application US/10727155
; Publication No. US20050049402A1
; GENERAL INFORMATION:
;  APPLICANT: John S. Babcook
;  APPLICANT:  Jaspal S. Kang
;  APPLICANT:  Orit Foord
;  APPLICANT:  Larry Green
;  APPLICANT:  Xiao Feng
;  APPLICANT:  Scott Klakamp
;  APPLICANT:  Mary Haak-Frendscho
;  APPLICANT:  Palaniswami Rathanaswami
;  APPLICANT:  Craig Pigott
;  APPLICANT:  Meina Liang
;  APPLICANT:  Rozanne Lee
;  APPLICANT:  Kathy Manchulencho
;  APPLICANT:  Raffaella Faggioni
;  APPLICANT:  Giorgio Senaldi
;  APPLICANT:  Qiaojuan Jane Su
;  TITLE OF INVENTION: ANTIBODIES DIRECTED TO TUMOR NECROSIS
;  TITLE OF INVENTION:  FACTOR AND USES THEREOF
;  FILE REFERENCE: ABGENIX.073A
;  CURRENT APPLICATION NUMBER: US/10/727,155
;  CURRENT FILING DATE:  2003-12-02
;  PRIOR APPLICATION NUMBER: 60/430729
;  PRIOR FILING DATE: 2002-12-02
;  NUMBER OF SEQ ID NOS: 320
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 92
;   LENGTH: 121
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-727-155-92

  Query Match             87.3%;  Score 537;  DB 17;  Length 121;
  Best Local Similarity   86.8%;  Pred. No. 8.8e-43;
  Matches  105;  Conservative    3;  Mismatches   11;  Indels    2;  Gaps    1;

Qy          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSSGMHWVRQAPGKGLEWVAXISYDGSRKYY 60
              |||||||||||||||||||||||||||||||| |||||||||||||||| | |||: |||
Db          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVIWYDGNNKYY 60

Qy         61 ADSVKGRFTISRDNSKNTLYLQMNSLTAXDTAVYYCAK--GVTGSPTLDYWGQGTLVTVS 118
              |||||||||||||||||||||||| | ||||||||:     |:|  ||||||||||||
Db         61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARESDYGGNPYFDYWGQGTLVTVS 120

Qy        119 S 119
              |
Db        121 S 121


RESULT 15
US-10-938-353-110
; Sequence 110, Application US/10938353
; Publication No. US20050059113A1
; GENERAL INFORMATION:
;  APPLICANT: BEDIAN, VAHE
;  APPLICANT:  DEVALARAJA, MADHAV NARASIMHA
;  APPLICANT:  FOLTZ, IAN
;  APPLICANT:  HAAK-FRENDSCHO, MARY
;  APPLICANT:  KELLERMANN, SIRID-AIMEE
;  APPLICANT:  LOW, JOSEPH EDWIN
;  APPLICANT:  MOBLEY, JAMES LESLIE
;  TITLE OF INVENTION: ANTIBODIES TO M-CSF
;  FILE REFERENCE: ABX-PF4
;  CURRENT APPLICATION NUMBER: US/10/938,353
;  CURRENT FILING DATE:  2004-09-09
;  PRIOR APPLICATION NUMBER: 60/502,163
;  PRIOR FILING DATE: 2003-09-10
;  NUMBER OF SEQ ID NOS: 117
;  SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 110
;   LENGTH: 117
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-938-353-110

  Query Match             87.1%;  Score 535.5;  DB 17;  Length 117;
  Best Local Similarity   88.2%;  Pred. No. 1.2e-42;
  Matches  105;  Conservative    2;  Mismatches    9;  Indels    3;  Gaps    1;

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Db          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVIWYDGSNKYY 60

Qy         61 ADSVKGRFTISRDNSKNTLYLQMNSLTAXDTAVYYCAKGVTGSPTLDYWGQGTLVTVSS 119
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Search completed: October 13, 2005, 03:02:47
Job time : 116.425 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: October 13, 2005, 02:37:04 ; Search time 19.4077 Seconds
(without alignments)
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	542.5	88.2	248	4	US-09-315-926A-80	Sequence 80, Appl
2	531	86.3	119	1	US-08-331-398A-46	Sequence 46, Appl
3	531	86.3	119	2	US-08-331-397B-46	Sequence 46, Appl
4	531	86.3	119	2	US-08-759-804A-46	Sequence 46, Appl
5	531	86.3	119	3	US-09-227-693-46	Sequence 46, Appl
6	525.5	85.4	463	4	US-09-472-087-1	Sequence 1, Appli
7	525.5	85.4	463	4	US-09-472-087-63	Sequence 63, Appl
8	525.5	85.4	463	4	US-09-472-087-64	Sequence 64, Appl
9	525	85.4	120	1	US-07-942-245-35	Sequence 35, Appl
10	521	84.7	225	4	US-09-456-090A-60	Sequence 60, Appl
11	521	84.7	225	4	US-09-456-090A-92	Sequence 92, Appl
12	521	84.7	225	4	US-09-453-234-60	Sequence 60, Appl
13	521	84.7	225	4	US-09-453-234-92	Sequence 92, Appl
14	520	84.6	225	4	US-09-456-090A-108	Sequence 108, App
15	520	84.6	225	4	US-09-453-234-108	Sequence 108, App
16	520	84.6	451	4	US-09-472-087-70	Sequence 70, Appl
17	517	84.1	464	4	US-09-472-087-2	Sequence 2, Appli
18	517	84.1	464	4	US-09-472-087-66	Sequence 66, Appl
19	515.5	83.8	463	4	US-09-472-087-4	Sequence 4, Appli
20	515.5	83.8	463	4	US-09-472-087-68	Sequence 68, Appl
21	515	83.7	225	4	US-09-456-090A-102	Sequence 102, App
22	515	83.7	225	4	US-09-456-090A-106	Sequence 106, App
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24	515	83.7	225	4	US-09-453-234-106	Sequence 106, App
25	513	83.4	123	4	US-09-560-198A-2	Sequence 2, Appli
26	513	83.4	225	4	US-09-456-090A-56	Sequence 56, Appl
27	513	83.4	225	4	US-09-456-090A-68	Sequence 68, Appl
28	513	83.4	225	4	US-09-456-090A-110	Sequence 110, App
29	513	83.4	225	4	US-09-453-234-56	Sequence 56, Appl
30	513	83.4	225	4	US-09-453-234-68	Sequence 68, Appl
31	513	83.4	225	4	US-09-453-234-110	Sequence 110, App
32	511	83.1	115	4	US-09-726-219A-167	Sequence 167, App
33	510	82.9	123	4	US-09-560-198A-10	Sequence 10, Appl
34	509	82.8	117	3	US-09-025-769B-24	Sequence 24, Appl
35	509	82.8	117	4	US-09-490-070A-24	Sequence 24, Appl
36	509	82.8	117	4	US-09-490-153-24	Sequence 24, Appl
37	509	82.8	117	4	US-09-490-324-24	Sequence 24, Appl
38	507	82.4	125	3	US-09-240-274-24	Sequence 24, Appl
39	507	82.4	225	4	US-09-456-090A-94	Sequence 94, Appl
40	507	82.4	225	4	US-09-453-234-94	Sequence 94, Appl
41	506	82.3	125	3	US-09-240-274-9	Sequence 9, Appli
42	505.5	82.2	124	4	US-09-424-840B-16	Sequence 16, Appl
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44	502.5	81.7	310	3	US-09-079-029-11	Sequence 11, Appl
45	502	81.6	116	1	US-08-211-202-141	Sequence 141, App

ALIGNMENTS

RESULT 1
US-09-315-926A-80
; Sequence 80, Application US/09315926A
; Patent No. 6498027
; GENERAL INFORMATION:
; APPLICANT: Es van, Helmuth
; APPLICANT: Havenga, Menzo
; APPLICANT: Verlinden, Stefan
; TITLE OF INVENTION: TARGETED DELIVERY THROUGH A CATIONIC AMINO ACID TRANSPORTER
; FILE REFERENCE: 2183-4080US
; CURRENT APPLICATION NUMBER: US/09/315,926A
; CURRENT FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: EP 99201593.3
; PRIOR FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: EP 98201693.3
; PRIOR FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 80
; LENGTH: 248
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Description of Artificial Sequence: phage
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(248)
; OTHER INFORMATION: /note="hCAT1 amino acid sequence"
US-09-315-926A-80

Query Match 88.2%; Score 542.5; DB 4; Length 248;
Best Local Similarity 87.5%; Pred. No. 1.9e-44;
Matches 105; Conservative 5; Mismatches 9; Indels 1; Gaps 1;

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Qy         61 ADSVKGRFTISRDNSKNTLYLQMNSLTAXDTAVYYCAKGVTGSPT-LDYWGQGTLVTVSS 119
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RESULT 2
US-08-331-398A-46
; Sequence 46, Application US/08331398A
; Patent No. 5608039
; GENERAL INFORMATION:
; APPLICANT: Pastan, Ira
; APPLICANT: Willingham, Mark

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;    APPLICANT:  FitzGerald, David
;    APPLICANT:  Brinkmann, Ulrich
;    APPLICANT:  Pai, Lee
;    TITLE OF INVENTION:  Single Chain B3 Antibody Fusion Proteins
;    TITLE OF INVENTION:  and Their Uses (as amended)
;    NUMBER OF SEQUENCES:  68
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend and Crew
;      STREET:  One Market Plaza, Steuart Street Plaza
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94105-1492
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/331,398A
;      FILING DATE:  28-OCT-1994
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/767,331
;      FILING DATE:  30-SEP-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/596,289
;      FILING DATE:  12-OCT-1990
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Hunter, Tom
;      REGISTRATION NUMBER:  38,498
;      REFERENCE/DOCKET NUMBER:  015280-126110US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 543-9600
;      TELEFAX:  (415) 543-5043
;  INFORMATION FOR SEQ ID NO:  46:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  119 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
;    FEATURE:
;      NAME/KEY:  Protein
;      LOCATION:  1..119
;      OTHER INFORMATION:  /note= "Human fetal immunoglobulin
;      OTHER INFORMATION:  56P1'CL Variable Heavy chain (V-H)"
US-08-331-398A-46

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  Matches  103;  Conservative    3;  Mismatches   13;  Indels    0;  Gaps    0;

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Qy         61 ADSVKGRFTISRDNSKNTLYLQMNSLTAXDTAVYYCAKGVTGSPTLDYWGQGTLVTVSS 119
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Db         61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARRSARTYYFDYWGQGTLVTVSS 119


RESULT 3
US-08-331-397B-46
; Sequence 46, Application US/08331397B
; Patent No. 5981726
;  GENERAL INFORMATION:
;    APPLICANT:  Pastan, Ira
;    APPLICANT:  Benhar, Itai
;    TITLE OF INVENTION:  Chimeric and Mutationally Stabilized Tumor-
;    TITLE OF INVENTION:  Specific Antibody Fragments, Fusion Proteins, and Uses
;    TITLE OF INVENTION:  Thereof
;    NUMBER OF SEQUENCES:  68
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend and Crew
;      STREET:  One Market Plaza, Steuart Street Plaza
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94105-1492
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/331,397B
;      FILING DATE:  28-OCT-1994
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/767,331
;      FILING DATE:  30-SEP-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/596,289
;      FILING DATE:  12-OCT-1990
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Hunter, Tom
;      REGISTRATION NUMBER:  38,498
;      REFERENCE/DOCKET NUMBER:  015280-126120US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 543-9600
;      TELEFAX:  (415) 543-5043
;  INFORMATION FOR SEQ ID NO:  46:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  119 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
;    FEATURE:
;      NAME/KEY:  Protein
;      LOCATION:  1..119
;      OTHER INFORMATION:  /note= "Human fetal immunoglobulin
;      OTHER INFORMATION:  56P1'CL Variable Heavy chain (V-H)"
US-08-331-397B-46

  Query Match             86.3%;  Score 531;  DB 2;  Length 119;
  Best Local Similarity   86.6%;  Pred. No. 1.1e-43;
  Matches  103;  Conservative    3;  Mismatches   13;  Indels    0;  Gaps    0;

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Qy         61 ADSVKGRFTISRDNSKNTLYLQMNSLTAXDTAVYYCAKGVTGSPTLDYWGQGTLVTVSS 119
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Db         61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARRSARTYYFDYWGQGTLVTVSS 119


RESULT 4
US-08-759-804A-46
; Sequence 46, Application US/08759804A
; Patent No. 5990296
;  GENERAL INFORMATION:
;    APPLICANT:  Pastan, Ira
;    APPLICANT:  Willingham, Mark
;    APPLICANT:  FitzGerald, David J.
;    APPLICANT:  Brinkmann, Ulrich
;    APPLICANT:  Pai, Lee
;    TITLE OF INVENTION:  Tumor-Specific Antibody Fragments,
;    TITLE OF INVENTION:  Fusion Proteins, and Uses Thereof
;    NUMBER OF SEQUENCES:  68
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend and Crew LLP
;      STREET:  Two Embarcadero Center, Eighth Floor
;      CITY:  San Francisco
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;       STATE:  California
;       COUNTRY:  USA
;       ZIP:  94111-3834
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.30
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/759,804A
;       FILING DATE:  03-DEC-1996
;       CLASSIFICATION:  536
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 08/331,398
;       FILING DATE:  28-OCT-1994
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 07/767,331
;       FILING DATE:  30-SEP-1991
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 07/596,289
;       FILING DATE:  12-OCT-1990
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Weber, Ellen L.
;       REGISTRATION NUMBER:  32,762
;       REFERENCE/DOCKET NUMBER:  015280-126140US
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (415) 576-0200
;       TELEFAX:  (415) 576-0300
;   INFORMATION FOR SEQ ID NO:  46:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  119 amino acids
;       TYPE:  amino acid
;       STRANDEDNESS:
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  protein
;     FEATURE:
;       NAME/KEY:  Protein
;       LOCATION:  1..119
;       OTHER INFORMATION:  /note= "Human fetal immunoglobulin
;       OTHER INFORMATION:  56P1'CL Variable Heavy chain (V-H)"
US-08-759-804A-46

  Query Match             86.3%;  Score 531;  DB 2;  Length 119;
  Best Local Similarity   86.6%;  Pred. No. 1.1e-43;
  Matches  103;  Conservative    3;  Mismatches   13;  Indels    0;  Gaps    0;

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Qy         61 ADSVKGRFTISRDNSKNTLYLQMNSLTAXDTAVYYCAKGVTGSPTLDYWGQGTLVTVSS 119
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Db         61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARRSARTYYFDYWGQGTLVTVSS 119


RESULT 5
US-09-227-693-46
; Sequence 46, Application US/09227693
; Patent No. 6287562
;  GENERAL INFORMATION:
;    APPLICANT:  PASTAN, Ira
;    APPLICANT:  BENHAR, Itai
;    APPLICANT:  PADLAN, Eduardo A.
;    APPLICANT:  JUNG, Sun-Hee
;    APPLICANT:  LEE, Byungkook
;    TITLE OF INVENTION:  HUMANIZED TUMOR-SPECIFIC ANTIBODY
;    TITLE OF INVENTION:  FRAGMENTS, FUSION PROTEINS, AND USES THEREOF
;    NUMBER OF SEQUENCES:  50
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend Khourie and Crew
;      STREET:  Steuart Street Tower, One Market Plaza
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  US
;      ZIP:  94105-1493
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/227,693
;      FILING DATE:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/331,396
;      FILING DATE:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/767,331
;      FILING DATE:  30-SEP-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/596,289
;      FILING DATE:  12-OCT-1990
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Weber, Ellen Lauver
;      REGISTRATION NUMBER:  32,762
;      REFERENCE/DOCKET NUMBER:  15280-126-1-3
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 543-9600
;      TELEFAX:  (415) 543-5043
;  INFORMATION FOR SEQ ID NO:  46:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  119 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
;    FEATURE:
;      NAME/KEY:  Protein
;      LOCATION:  1..119
;      OTHER INFORMATION:  /note= "Human fetal immunoglobulin
;      OTHER INFORMATION:  56P1'CL VH region"
US-09-227-693-46

  Query Match             86.3%;  Score 531;  DB 3;  Length 119;
  Best Local Similarity   86.6%;  Pred. No. 1.1e-43;
  Matches  103;  Conservative    3;  Mismatches   13;  Indels    0;  Gaps    0;

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Qy         61 ADSVKGRFTISRDNSKNTLYLQMNSLTAXDTAVYYCAKGVTGSPTLDYWGQGTLVTVSS 119
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Db         61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARRSARTYYFDYWGQGTLVTVSS 119


RESULT 6
US-09-472-087-1
; Sequence 1, Application US/09472087
; Patent No. 6682736
; GENERAL INFORMATION:
;  APPLICANT: HANSON, DOUGLAS C.
;  APPLICANT:  NEVEU, MARK J.
;  APPLICANT:  MUELLER, EILLEN E.
;  APPLICANT:  HANKE, JEFFREY H.
;  APPLICANT:  GILMAN, STEVEN C.
;  APPLICANT:  DAVIS, C. GEOFFREY
;  APPLICANT:  CORVALAN, JOSE R.
;  TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
;  FILE REFERENCE: ABX-PF1
;  CURRENT APPLICATION NUMBER: US/09/472,087
;  CURRENT FILING DATE:  1999-12-23
;  PRIOR APPLICATION NUMBER: 60/113,647
;  PRIOR FILING DATE: 1998-12-23
;  NUMBER OF SEQ ID NOS: 147
;  SOFTWARE: PatentIn Ver. 2.1
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; SEQ ID NO 1
;   LENGTH: 463
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-472-087-1

  Query Match             85.4%;  Score 525.5;  DB 4;  Length 463;
  Best Local Similarity   86.6%;  Pred. No. 1.6e-42;
  Matches  103;  Conservative    2;  Mismatches   13;  Indels    1;  Gaps    1;

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Qy         61 ADSVKGRFTISRDNSKNTLYLQMNSLTAXDTAVYYCAKGVTGSPTLDYWGQGTLVTVSS 119
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RESULT 7
US-09-472-087-63
; Sequence 63, Application US/09472087
; Patent No. 6682736
; GENERAL INFORMATION:
;  APPLICANT: HANSON, DOUGLAS C.
;  APPLICANT:  NEVEU, MARK J.
;  APPLICANT:  MUELLER, EILLEN E.
;  APPLICANT:  HANKE, JEFFREY H.
;  APPLICANT:  GILMAN, STEVEN C.
;  APPLICANT:  DAVIS, C. GEOFFREY
;  APPLICANT:  CORVALAN, JOSE R.
;  TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
;  FILE REFERENCE: ABX-PF1
;  CURRENT APPLICATION NUMBER: US/09/472,087
;  CURRENT FILING DATE:  1999-12-23
;  PRIOR APPLICATION NUMBER: 60/113,647
;  PRIOR FILING DATE: 1998-12-23
;  NUMBER OF SEQ ID NOS: 147
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 63
;   LENGTH: 463
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-472-087-63

  Query Match             85.4%;  Score 525.5;  DB 4;  Length 463;
  Best Local Similarity   86.6%;  Pred. No. 1.6e-42;
  Matches  103;  Conservative    2;  Mismatches   13;  Indels    1;  Gaps    1;

Qy          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSSGMHWVRQAPGKGLEWVAXISYDGSRKYY 60
              |||||||||||||||||||||||| |||||||| |||||||||||||||| | |||  |||
Db         20 QVQLVESGGGVVQPGRSLRLSCVASGFTFSSHGMHWVRQAPGKGLEWVAVIWYDGRNKYY 79

Qy         61 ADSVKGRFTISRDNSKNTLYLQMNSLTAXDTAVYYCAKGVTGSPTLDYWGQGTLVTVSS 119
              ||||||||||||||||||:|||||| | ||||||||:|    |  ||||||||||||||
Db         80 ADSVKGRFTISRDNSKNTLFLQMNSLRAEDTAVYYCARGGHFGP-FDYWGQGTLVTVSS 137


RESULT 8
US-09-472-087-64
; Sequence 64, Application US/09472087
; Patent No. 6682736
; GENERAL INFORMATION:
;  APPLICANT: HANSON, DOUGLAS C.
;  APPLICANT:  NEVEU, MARK J.
;  APPLICANT:  MUELLER, EILLEN E.
;  APPLICANT:  HANKE, JEFFREY H.
;  APPLICANT:  GILMAN, STEVEN C.
;  APPLICANT:  DAVIS, C. GEOFFREY
;  APPLICANT:  CORVALAN, JOSE R.
;  TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
;  FILE REFERENCE: ABX-PF1
;  CURRENT APPLICATION NUMBER: US/09/472,087
;  CURRENT FILING DATE:  1999-12-23
;  PRIOR APPLICATION NUMBER: 60/113,647
;  PRIOR FILING DATE: 1998-12-23
;  NUMBER OF SEQ ID NOS: 147
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 64
;   LENGTH: 463
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-472-087-64

  Query Match             85.4%;  Score 525.5;  DB 4;  Length 463;
  Best Local Similarity   86.6%;  Pred. No. 1.6e-42;
  Matches  103;  Conservative    2;  Mismatches   13;  Indels    1;  Gaps    1;

Qy          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSSGMHWVRQAPGKGLEWVAXISYDGSRKYY 60
              |||||||||||||||||||||||| |||||||| |||||||||||||||| | |||  |||
Db         20 QVQLVESGGGVVQPGRSLRLSCVASGFTFSSHGMHWVRQAPGKGLEWVAVIWYDGRNKYY 79

Qy         61 ADSVKGRFTISRDNSKNTLYLQMNSLTAXDTAVYYCAKGVTGSPTLDYWGQGTLVTVSS 119
              ||||||||||||||||||:|||||| | ||||||||:|    |  ||||||||||||||
Db         80 ADSVKGRFTISRDNSKNTLFLQMNSLRAEDTAVYYCARGGHFGP-FDYWGQGTLVTVSS 137


RESULT 9
US-07-942-245-35
; Sequence 35, Application US/07942245
; Patent No. 5639641
; GENERAL INFORMATION:
;    APPLICANT:  PEDERSEN, Jan T.
;    APPLICANT:  SEARLE,   Stephen M.J.
;    APPLICANT:  REES,     Anthony R.
;    APPLICANT:  ROGUSKA,  Michael A.
;    APPLICANT:  GUILD,    Braydon C.
;    TITLE OF INVENTION:  SURFACE RESIDUE VENEERING OF RODENT
;    TITLE OF INVENTION:  ANTIBODIES
;    NUMBER OF SEQUENCES:  522
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Sughrue, Mion, Zinn, Macpeak & Seas
;      STREET:  2100 Pensylvania Avenue, N.W.
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  United States
;      ZIP:  20037-3202
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  HP 9000/700 Workstation
;      OPERATING SYSTEM:  UNIX
;      SOFTWARE:  In house
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/942,245
;      FILING DATE:  09-SEP-1992
;      CLASSIFICATION:  530
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202) 293-7060
;      TELEFAX:  (202) 293-7860
;      TELEX:  6491103
;  INFORMATION FOR SEQ ID NO:  35:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  120 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-07-942-245-35

  Query Match             85.4%;  Score 525;  DB 1;  Length 120;
  Best Local Similarity   86.7%;  Pred. No. 4.2e-43;
  Matches  104;  Conservative    1;  Mismatches   13;  Indels    2;  Gaps    1;

Qy          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSSGMHWVRQAPGKGLEWVAXISYDGSRKYY 60
              |||||||||||||||||||||||||||||| |||||||||||||| |||||| |||
Db          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYY 60
```

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Qy         61 ADSVKGRFTISRDNSKNTLYLQMNSLTAXDTAVYYCAKGVT--GSPTLDYWGQGTLVTVS 118
              ||||||||||||||||||||||||| | ||||||||:     |    ||||||||||||
Db         61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDRKDWGWALFDYWGQGTLVTVS 120


RESULT 10
US-09-456-090A-60
; Sequence 60, Application US/09456090A
; Patent No. 6680209
; GENERAL INFORMATION:
;  APPLICANT: Buechler, Joe
;  APPLICANT:  Valkirs, Gunars
;  APPLICANT:  Gray, Jeff
;  APPLICANT:  Lonberg, Nils
;  TITLE OF INVENTION: HUMAN ANTIBODIES AS DIAGNOSTIC REAGENTS
;  FILE REFERENCE: 020015-000200US
;  CURRENT APPLICATION NUMBER: US/09/456,090A
;  CURRENT FILING DATE:  1999-12-06
;  NUMBER OF SEQ ID NOS: 110
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 60
;   LENGTH: 225
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   OTHER INFORMATION: M1-5H
US-09-456-090A-60

  Query Match             84.7%;  Score 521;  DB 4;  Length 225;
  Best Local Similarity   85.7%;  Pred. No. 2e-42;
  Matches  102;  Conservative    2;  Mismatches   13;  Indels    2;  Gaps    1;

Qy          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSSGMHWVRQAPGKGLEWVAXISYDGSRKYY 60
              ||||||||||||||||||||||||||||||  ||||||||||||||||  |:|||  |||
Db          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSYYGMHWVRQAPGKGLEWVTLITYDGDNKYY 60

Qy         61 ADSVKGRFTISRDNSKNTLYLQMNSLTAXDTAVYYCAKGVTGSPTLDYWGQGTLVTVSS 119
              ||||||||||||||||||||||||| | ||||||||:    |    ||||||||||||
Db         61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAR--DGIGYFDYWGQGTLVTVSS 117


RESULT 11
US-09-456-090A-92
; Sequence 92, Application US/09456090A
; Patent No. 6680209
; GENERAL INFORMATION:
;  APPLICANT: Buechler, Joe
;  APPLICANT:  Valkirs, Gunars
;  APPLICANT:  Gray, Jeff
;  APPLICANT:  Lonberg, Nils
;  TITLE OF INVENTION: HUMAN ANTIBODIES AS DIAGNOSTIC REAGENTS
;  FILE REFERENCE: 020015-000200US
;  CURRENT APPLICATION NUMBER: US/09/456,090A
;  CURRENT FILING DATE:  1999-12-06
;  NUMBER OF SEQ ID NOS: 110
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 92
;   LENGTH: 225
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   OTHER INFORMATION: M2-11H
US-09-456-090A-92

  Query Match             84.7%;  Score 521;  DB 4;  Length 225;
  Best Local Similarity   85.7%;  Pred. No. 2e-42;
  Matches  102;  Conservative    2;  Mismatches   13;  Indels    2;  Gaps    1;

Qy          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSSGMHWVRQAPGKGLEWVAXISYDGSRKYY 60
              ||||||||||||||||||||||||||||||  ||||||||||||||||  |:|||  |||
Db          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSYYGMHWVRQAPGKGLEWVTLITYDGDNKYY 60

Qy         61 ADSVKGRFTISRDNSKNTLYLQMNSLTAXDTAVYYCAKGVTGSPTLDYWGQGTLVTVSS 119
              ||||||||||||||||||||||||| | ||||||||:    |    ||||||||||||
Db         61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAR--DGIGYFDYWGQGTLVTVSS 117


RESULT 12
US-09-453-234-60
; Sequence 60, Application US/09453234
; Patent No. 6794132
; GENERAL INFORMATION:
;  APPLICANT: Buechler, Joe
;  APPLICANT:  Valkirs, Gunars
;  APPLICANT:  Gray, Jeff
;  APPLICANT:  Lonberg, Nils
;  APPLICANT:  Biosite Diagnostics, Inc.
;  APPLICANT:  GenPharm International
;  TITLE OF INVENTION: Human Antibodies
;  FILE REFERENCE: 020015-000110US
;  CURRENT APPLICATION NUMBER: US/09/453,234
;  CURRENT FILING DATE:  1999-12-01
;  PRIOR APPLICATION NUMBER: US 60/157,415
;  PRIOR FILING DATE: 1999-10-02
;  NUMBER OF SEQ ID NOS: 112
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 60
;   LENGTH: 225
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   OTHER INFORMATION: M1-5H
US-09-453-234-60

  Query Match             84.7%;  Score 521;  DB 4;  Length 225;
  Best Local Similarity   85.7%;  Pred. No. 2e-42;
  Matches  102;  Conservative    2;  Mismatches   13;  Indels    2;  Gaps    1;

Qy          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSSGMHWVRQAPGKGLEWVAXISYDGSRKYY 60
              ||||||||||||||||||||||||||||||  ||||||||||||||||  |:|||  |||
Db          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSYYGMHWVRQAPGKGLEWVTLITYDGDNKYY 60

Qy         61 ADSVKGRFTISRDNSKNTLYLQMNSLTAXDTAVYYCAKGVTGSPTLDYWGQGTLVTVSS 119
              ||||||||||||||||||||||||| | ||||||||:    |    ||||||||||||
Db         61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAR--DGIGYFDYWGQGTLVTVSS 117


RESULT 13
US-09-453-234-92
; Sequence 92, Application US/09453234
; Patent No. 6794132
; GENERAL INFORMATION:
;  APPLICANT: Buechler, Joe
;  APPLICANT:  Valkirs, Gunars
;  APPLICANT:  Gray, Jeff
;  APPLICANT:  Lonberg, Nils
;  APPLICANT:  Biosite Diagnostics, Inc.
;  APPLICANT:  GenPharm International
;  TITLE OF INVENTION: Human Antibodies
;  FILE REFERENCE: 020015-000110US
;  CURRENT APPLICATION NUMBER: US/09/453,234
;  CURRENT FILING DATE:  1999-12-01
;  PRIOR APPLICATION NUMBER: US 60/157,415
;  PRIOR FILING DATE: 1999-10-02
;  NUMBER OF SEQ ID NOS: 112
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 92
;   LENGTH: 225
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   OTHER INFORMATION: M2-11H
US-09-453-234-92

  Query Match             84.7%;  Score 521;  DB 4;  Length 225;
  Best Local Similarity   85.7%;  Pred. No. 2e-42;
  Matches  102;  Conservative    2;  Mismatches   13;  Indels    2;  Gaps    1;

Qy          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSSGMHWVRQAPGKGLEWVAXISYDGSRKYY 60
              ||||||||||||||||||||||||||||||  ||||||||||||||||  |:|||  |||
```

```
Db          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSYYGMHWVRQAPGKGLEWVTLITYDGDNKYY 60

Qy         61 ADSVKGRFTISRDNSKNTLYLQMNSLTAXDTAVYYCAKGVTGSPTLDYWGQGTLVTVSS 119
              |||||||||||||||||||||||| | ||||||||:   |    ||||||||||||
Db         61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAR--DGIGYFDYWGQGTLVTVSS 117


RESULT 14
US-09-456-090A-108
; Sequence 108, Application US/09456090A
; Patent No. 6680209
; GENERAL INFORMATION:
;  APPLICANT: Buechler, Joe
;  APPLICANT:  Valkirs, Gunars
;  APPLICANT:  Gray, Jeff
;  APPLICANT:  Lonberg, Nils
;  TITLE OF INVENTION: HUMAN ANTIBODIES AS DIAGNOSTIC REAGENTS
;  FILE REFERENCE: 020015-000200US
;  CURRENT APPLICATION NUMBER: US/09/456,090A
;  CURRENT FILING DATE:  1999-12-06
;  NUMBER OF SEQ ID NOS: 110
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 108
;   LENGTH: 225
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   OTHER INFORMATION: M2-34H
US-09-456-090A-108

  Query Match             84.6%;  Score 520;  DB 4;  Length 225;
  Best Local Similarity   85.7%;  Pred. No. 2.5e-42;
  Matches  102;  Conservative    2;  Mismatches   13;  Indels    2;  Gaps    1;

Qy          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSSGMHWVRQAPGKGLEWVAXISYDGSRKYY 60
              |||||||||||||||||||||||||||||  |:||||| ||||||||  |||||| |||
Db          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSYYGIHWVRQVPGKGLEWVVLISYDGSNKYY 60

Qy         61 ADSVKGRFTISRDNSKNTLYLQMNSLTAXDTAVYYCAKGVTGSPTLDYWGQGTLVTVSS 119
              |||||||||||||||||||||||| | ||||||||:   |    ||||||||||||
Db         61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDWIG--YFDYWGQGTLVTVSS 117


RESULT 15
US-09-453-234-108
; Sequence 108, Application US/09453234
; Patent No. 6794132
; GENERAL INFORMATION:
;  APPLICANT: Buechler, Joe
;  APPLICANT:  Valkirs, Gunars
;  APPLICANT:  Gray, Jeff
;  APPLICANT:  Lonberg, Nils
;  APPLICANT:  Biosite Diagnostics, Inc.
;  APPLICANT:  GenPharm International
;  TITLE OF INVENTION: Human Antibodies
;  FILE REFERENCE: 020015-000110US
;  CURRENT APPLICATION NUMBER: US/09/453,234
;  CURRENT FILING DATE:  1999-12-01
;  PRIOR APPLICATION NUMBER: US 60/157,415
;  PRIOR FILING DATE: 1999-10-02
;  NUMBER OF SEQ ID NOS: 112
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 108
;   LENGTH: 225
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   OTHER INFORMATION: M2-34H
US-09-453-234-108

  Query Match             84.6%;  Score 520;  DB 4;  Length 225;
  Best Local Similarity   85.7%;  Pred. No. 2.5e-42;
  Matches  102;  Conservative    2;  Mismatches   13;  Indels    2;  Gaps    1;

Qy          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSSGMHWVRQAPGKGLEWVAXISYDGSRKYY 60
              |||||||||||||||||||||||||||||  |:||||| ||||||||  |||||| |||
Db          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSYYGIHWVRQVPGKGLEWVVLISYDGSNKYY 60

Qy         61 ADSVKGRFTISRDNSKNTLYLQMNSLTAXDTAVYYCAKGVTGSPTLDYWGQGTLVTVSS 119
              |||||||||||||||||||||||| | ||||||||:   |    ||||||||||||
Db         61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDWIG--YFDYWGQGTLVTVSS 117


Search completed: October 13, 2005, 02:45:19
Job time : 20.4077 secs
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Protein Sequence Searches - February 2005

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.

- If you encounter an accession number from an older search run against UniProt (results file extension **.rup)** that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (UniPARC) at:

  http://www.pir.uniprot.org/database/archive.shtml

If you have any questions regarding this information or your results, please contact any STIC searcher.

When submitting sequence search results for scanning into IFW, please include a copy of this attachment to assist any future Examiners or members of the public who may encounter UniProt temporary accession numbers.

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: October 13, 2005, 02:45:26 ; Search time 118.489 Seconds
(without alignments)
514.286 Million cell updates/sec

Title: US-10-010-729A-7
Perfect score: 615
Sequence: 1 QVQLVESGGGVVQPGRSLRL.....VTGSPTLDYWGQGTLVTVSS 119

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	537.5	87.4	613	2	Q8WUK1	Q8wuk1 homo sapien
2	525	85.4	116	2	Q9UL93	Q9ul93 homo sapien
3	523	85.0	113	2	Q9UL90	Q9ul90 homo sapien
4	513	83.4	240	2	Q65ZC9	Q65zc9 homo sapien
5	490.5	79.8	122	2	Q9UL84	Q9ul84 homo sapien
6	489.5	79.6	122	1	HV3G_HUMAN	P01768 homo sapien
7	482.5	78.5	147	2	Q9Y509	Q9y509 homo sapien
8	482	78.4	121	1	HV3J_HUMAN	P01771 homo sapien
9	474	77.1	121	2	Q9UL71	Q9ul71 homo sapien
10	471	76.6	493	2	Q6GMX2	Q6gmx2 homo sapien
11	468	76.1	597	2	Q96BB9	Q96bb9 homo sapien
12	467.5	76.0	122	1	HV3H_HUMAN	P01769 homo sapien
13	467	75.9	478	2	Q6PI81	Q6pi81 homo sapien
14	464.5	75.5	544	2	Q6PJ95	Q6pj95 homo sapien
15	464	75.4	119	1	HV3I_HUMAN	P01770 homo sapien
16	462	75.1	470	2	Q6PJA4	Q6pja4 homo sapien
17	460.5	74.9	118	2	Q9UL72	Q9ul72 homo sapien
18	460	74.8	464	2	Q6MZU6	Q6mzu6 homo sapien
19	459.5	74.7	573	2	Q8WU38	Q8wu38 homo sapien
20	458.5	74.6	116	1	HV3T_HUMAN	P01781 homo sapien
21	458	74.5	493	2	Q8NCL6	Q8ncl6 homo sapien
22	456.5	74.2	118	2	Q9UL91	Q9ul91 homo sapien
23	453	73.7	472	2	Q6N089	Q6n089 homo sapien
24	452.5	73.6	126	1	HV3K_HUMAN	P01772 homo sapien
25	452	73.5	466	2	Q6IN78	Q6in78 homo sapien
26	450	73.2	519	2	Q6N092	Q6n092 homo sapien
27	449	73.0	119	1	HV3L_HUMAN	P01773 homo sapien
28	446.5	72.6	479	2	Q6MZV6	Q6mzv6 homo sapien
29	443.5	72.1	473	2	Q6MZV7	Q6mzv7 homo sapien
30	442.5	72.0	112	2	Q9HCC1	Q9hcc1 homo sapien
31	442.5	72.0	606	2	Q6GMY2	Q6gmy2 homo sapien
32	442	71.9	482	2	Q7Z351	Q7z351 homo sapien
33	441.5	71.8	114	1	HV3B_HUMAN	P01763 homo sapien
34	438.5	71.3	136	1	HV16_MOUSE	P01783 mus musculu
35	436	70.9	499	2	Q8N5K4	Q8n5k4 homo sapien
36	435.5	70.8	465	2	Q6P6C4	Q6p6c4 homo sapien
37	434.5	70.7	487	2	Q99KA4	Q99ka4 mus musculu
38	433	70.4	480	2	Q6N094	Q6n094 homo sapien
39	430.5	70.0	473	2	Q91Z05	Q91z05 mus musculu
40	429	69.8	119	2	Q920E7	Q920e7 mus musculu
41	426	69.3	485	2	Q6PDB8	Q6pdb8 mus musculu
42	425.5	69.2	483	2	Q6MZX9	Q6mzx9 homo sapien
43	420.5	68.4	494	2	Q96K68	Q96k68 homo sapien
44	419.5	68.2	119	1	HV3M_HUMAN	P01774 homo sapien
45	419.5	68.2	475	2	Q6MZQ6	Q6mzq6 homo sapien

ALIGNMENTS

RESULT 1
Q8WUK1
ID Q8WUK1 PRELIMINARY; PRT; 613 AA.
AC Q8WUK1;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE IGHM protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RA Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
DR EMBL; BC020240; AAH20240.1; -.
DR PIR; F36005; F36005.
DR PIR; G36005; G36005.
DR PIR; PH1642; PH1642.
DR PIR; PH1643; PH1643.
DR PIR; PH1645; PH1645.
DR PIR; PH1646; PH1646.
DR PIR; PL0098; PL0098.
DR PIR; PL0120; PL0120.
DR PIR; S15590; S15590.
DR PIR; S31116; S31116.
DR PIR; S31119; S31119.
DR PIR; S70442; S70442.

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DR   HSSP; P01861; 1ADQ.
DR   Pfam; PF07654; C1-set; 4.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 5.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_3.
SQ   SEQUENCE   613 AA;  67295 MW;  60C7F5950671E315 CRC64;

  Query Match             87.4%;  Score 537.5;  DB 2;  Length 613;
  Best Local Similarity   88.3%;  Pred. No. 1.5e-49;
  Matches  106;  Conservative    2;  Mismatches   11;  Indels    1;  Gaps    1;

Qy          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSSGMHWVRQAPGKGLEWVAXISYDGSRKYY 60
              |||||||||||||||||||||||||||||| |||||||||||||||| |||||| |||
Db         20 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVISYDGSNKYY 79

Qy         61 ADSVKGRFTISRDNSKNTLYLQMNSLTAXDTAVYYCAKGVT-GSPTLDYWGQGTLVTVSS 119
              |||||||||||||||||||||||| | |||||||||  : |  | | |||||:|||||
Db         80 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKDWSEGVETFDIWGQGTMVTVSS 139


RESULT 2
Q9UL93
ID   Q9UL93      PRELIMINARY;      PRT;   116 AA.
AC   Q9UL93;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Myosin-reactive immunoglobulin heavy chain variable region
DE   (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
RA   Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA   Young D.C.;
RT   "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT   fetus.";
RL   Clin. Immunol. Immunopathol. 87:184-192(1998).
DR   EMBL; AF035021; AAD56257.1; -.
DR   PIR; PH1644; PH1644.
DR   PIR; PL0120; PL0120.
DR   HSSP; P01772; 2FB4.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
FT   NON_TER       1      1
FT   NON_TER     116    116
SQ   SEQUENCE   116 AA;  12434 MW;  0DA0348154DD6061 CRC64;

  Query Match             85.4%;  Score 525;  DB 2;  Length 116;
  Best Local Similarity   88.1%;  Pred. No. 5e-49;
  Matches  104;  Conservative    1;  Mismatches   11;  Indels    2;  Gaps    1;

Qy          2 VQLVESGGGVVQPGRSLRLSCAASGFTFSSSGMHWVRQAPGKGLEWVAXISYDGSRKYYA 61
              |||||||||||||||||||||||||||||  |||||||||||||||| ||||||  ||||
Db          1 VQLVESGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYYA 60

Qy         62 DSVKGRFTISRDNSKNTLYLQMNSLTAXDTAVYYCAKGVTGSPTLDYWGQGTLVTVSS 119
              ||||||||||||||||||||||| | |||:|||| |  |    | ||||||||||||
Db         61 DSVKGRFTISRDNSKNTLYLQMNSLRAEDTAMYYCAGG--GGLGLGYWGQGTLVTVSS 116


RESULT 3
Q9UL90
ID   Q9UL90      PRELIMINARY;      PRT;   113 AA.
AC   Q9UL90;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Myosin-reactive immunoglobulin heavy chain variable region
DE   (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
RA   Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA   Young D.C.;
RT   "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT   fetus.";
RL   Clin. Immunol. Immunopathol. 87:184-192(1998).
DR   EMBL; AF035024; AAD56260.1; -.
DR   PIR; S78486; S78486.
DR   HSSP; P01772; 2FB4.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
FT   NON_TER       1      1
FT   NON_TER     113    113
SQ   SEQUENCE   113 AA;  12437 MW;  ED57FDD19086D07F CRC64;

  Query Match             85.0%;  Score 523;  DB 2;  Length 113;
  Best Local Similarity   86.6%;  Pred. No. 8.1e-49;
  Matches  103;  Conservative    2;  Mismatches    8;  Indels    6;  Gaps    1;

Qy          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSSGMHWVRQAPGKGLEWVAXISYDGSRKYY 60
              :|||||||||||||| |||||||||||||||| |||||||||||||||| | |||| |||
Db          1 EVQLVESGGGVVQPGGSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAFIRYDGSNKYY 60

Qy         61 ADSVKGRFTISRDNSKNTLYLQMNSLTAXDTAVYYCAKGVTGSPTLDYWGQGTLVTVSS 119
              |||||||||||||||||||||||| | |||||||||       |:||||||||||||
Db         61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAK------DLNYWGQGTLVTVSS 113


RESULT 4
Q65ZC9
ID   Q65ZC9      PRELIMINARY;      PRT;   240 AA.
AC   Q65ZC9;
DT   25-OCT-2004 (TrEMBLrel. 28, Created)
DT   25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT   25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE   Single-chain Fv (Fragment).
GN   Name=scFv;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C1q/7;
RX   MEDLINE=97362799; PubMed=9219263;
RA   Kontermann R.E., Wing M.G., Winter G.;
RT   "Complement recruitment using bispecific diabodies.";
RL   Nat. Biotechnol. 15:629-631(1997).
DR   EMBL; Y13056; CAA73499.1; -.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00406; IGv; 2.
DR   PROSITE; PS50835; IG_LIKE; 2.
FT   NON_TER       1      1
FT   NON_TER     240    240
SQ   SEQUENCE   240 AA;  25569 MW;  FDCFD3645F64B373 CRC64;

  Query Match             83.4%;  Score 513;  DB 2;  Length 240;
  Best Local Similarity   84.9%;  Pred. No. 2.3e-47;
  Matches  101;  Conservative    5;  Mismatches   11;  Indels    2;  Gaps    1;
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Qy          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSSGMHWVRQAPGKGLEWVAXISYDGSRKYY 60
              |||||:||||:|||| |||||||||||||||| |||||||||||||||||| |||||| |||
Db          1 QVQLVQSGGGLVQPGGSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVISYDGSNKYY 60

Qy         61 ADSVKGRFTISRDNSKNTLYLQMNSLTAXDTAVYYCAKGVTGSPTLDYWGQGTLVTVSS 119
              |||||||||||||||||||||||| | ||||||||:      :|| ||:||||||||
Db         61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAR--DWGDSLDPWGKGTLVTVSS 117


RESULT 5
Q9UL84
ID   Q9UL84      PRELIMINARY;      PRT;   122 AA.
AC   Q9UL84;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Myosin-reactive immunoglobulin heavy chain variable region
DE   (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
RA   Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA   Young D.C.;
RT   "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT   fetus.";
RL   Clin. Immunol. Immunopathol. 87:184-192(1998).
DR   EMBL; AF035030; AAD56266.1; -.
DR   HSSP; P01772; 2FB4.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
FT   NON_TER       1      1
FT   NON_TER     122    122
SQ   SEQUENCE   122 AA;  13579 MW;  36054D41366545B8 CRC64;

  Query Match             79.8%;  Score 490.5;  DB 2;  Length 122;
  Best Local Similarity   80.3%;  Pred. No. 3e-45;
  Matches   98;  Conservative    4;  Mismatches   17;  Indels    3;  Gaps    1;

Qy          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSSGMHWVRQAPGKGLEWVAXISYDGSRKYY 60
              :|||||||||||||||||||||||| ||||: |||||||||||||||| || ||| |:|
Db          1 EVQLVESGGGVVQPGRSLRLSCAASRFTFSNYGMHWVRQAPGKGLEWVAAISNDGSNKFY 60

Qy         61 ADSVKGRFTISRDNSKNTLYLQMNSLTAXDTAVYYCAKGVTG---SPTLDYWGQGTLVTV 117
              |||||||||| |||||| : |||||| | |||||||||    |        ||||||||||
Db         61 ADSVKGRFTIFRDNSKNMMDLQMNSLRAEDTAVYYCAKDERGRLVGTYFDYWGQGTLVTV 120

Qy        118 SS 119
              ||
Db        121 SS 122


RESULT 6
HV3G_HUMAN
ID   HV3G_HUMAN     STANDARD;      PRT;   122 AA.
AC   P01768;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Ig heavy chain V-III region CAM.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=81013859; PubMed=6774332;
RA   Lehman D.W., Putnam F.W.;
RT   "Amino acid sequence of the variable region of a human mu chain:
RT   location of a possible JH segment.";
RL   Proc. Natl. Acad. Sci. U.S.A. 77:3239-3243(1980).
CC   -!- MISCELLANEOUS: This mu chain was isolated from the plasma of a
CC       patient with macroglobulinemia.
CC   -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR   PIR; A02051; M3HUAM.
DR   HSSP; P01772; 2FB4.
DR   GO; GO:0005576; C:extracellular; NAS.
DR   GO; GO:0003823; F:antigen binding; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Direct protein sequencing; Immunoglobulin V region;
KW   Pyrrolidone carboxylic acid.
FT   DOMAIN        1    112       Ig-like.
FT   MOD_RES       1      1       Pyrrolidone carboxylic acid.
FT   NON_TER     122    122
SQ   SEQUENCE   122 AA;  13668 MW;  A42D0F17D252F1C2 CRC64;

  Query Match             79.6%;  Score 489.5;  DB 1;  Length 122;
  Best Local Similarity   77.0%;  Pred. No. 3.8e-45;
  Matches   94;  Conservative   11;  Mismatches   14;  Indels    3;  Gaps    2;

Qy          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSSGMHWVRQAPGKGLEWVAXISYDGSRKYY 60
              ||:|||||||||:|||||||||||||||:  |||||| ||||||||| |||:|  |||
Db          1 QVELVESGGGVVZPGRSLRLSCAASGFTFSNYAMHWVRQPPGKGLEWVAVISYBGBBKYY 60

Qy         61 ADSVKGRFTISRDNSKNTLYLQMNSLTAXDTAVYYCAKG--VTGS-PTLDYWGQGTLVTV 117
              |:||||||||||:||:||||||||| | :|||||||:   : |     :||||||||||
Db         61 ABSVKGRFTISRDBSKBTLYLQMNSLRAEBTAVYYCARDRPLYGBYRAFNYWGQGTLVTV 120

Qy        118 SS 119
              ||
Db        121 SS 122


RESULT 7
Q9Y509
ID   Q9Y509      PRELIMINARY;      PRT;   147 AA.
AC   Q9Y509;
DT   01-NOV-1999 (TrEMBLrel. 12, Created)
DT   01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   VH3 protein (Fragment).
GN   Name=VH3;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=96071149; PubMed=7475288;
RA   Cao J., Vescio R.A., Rettig M.B., Hong C.H., Kim A., Lee J.C.,
RA   Lichtenstein A.K., Berenson J.R.;
RT   "A CD10-positive subset of malignant cells is identified in multiple
RT   myeloma using PCR with patient-specific immunoglobulin gene primers.";
RL   Leukemia 9:1948-1953(1995).
DR   EMBL; S80860; AAD14339.1; -.
DR   HSSP; P01842; 1AQK.
DR   GO; GO:0005887; C:integral to plasma membrane; NAS.
DR   GO; GO:0016066; P:cellular defense response (sensu Vertebrata); NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
FT   NON_TER     147    147
SQ   SEQUENCE   147 AA;  15768 MW;  8489FCAAA7BC925C CRC64;
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  Query Match             78.5%;  Score 482.5;  DB 2;  Length 147;
  Best Local Similarity   75.8%;  Pred. No. 2.7e-44;
  Matches   97;  Conservative    6;  Mismatches   14;  Indels   11;  Gaps    2;

Qy          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSSGMHWVRQAPGKGLEWVAXISYDGSRKYY 60
              || |||||||||||:|||||| |||||||: || ||||||||||:||| |||||| :||
Db          1 QVHLVESGGGVVQPGKSLRLSCEASGFTFSTYGMSWVRQAPGKGLDWVALISYDGSTQYY 60

Qy         61 ADSVKGRFTISRDNSKNTLYLQMNSLTAXDTAVYYCAKGVTGS---------PTLDYWGQ 111
              | ||||||||||||||||||||| ||   |||||||||   |:         :|||||
Db         61 AGSVKGRFTISRDNSKNTLYLQMTSLRVEDTAVYYCAK--DGNYFDSVGYYYAGIDYWGQ 118

Qy        112 GTLVTVSS 119
              ||||||||
Db        119 GTLVTVSS 126


RESULT 8
HV3J_HUMAN
ID   HV3J_HUMAN     STANDARD;      PRT;   121 AA.
AC   P01771;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Ig heavy chain V-III region HIL.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=79124695; PubMed=420800;
RA   Chiu Y.-Y.H., Lopez de Castro J.A., Poljak R.J.;
RT   "Amino acid sequence of the VH region of human myeloma
RT   cryoimmunoglobulin IgG Hil.";
RL   Biochemistry 18:553-560(1979).
CC   -!- MISCELLANEOUS: This chain was isolated from an IgG1 myeloma
CC       protein.
CC   -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR   PIR; A02054; G1HUHL.
DR   HSSP; P01772; 2FB4.
DR   GO; GO:0005576; C:extracellular; NAS.
DR   GO; GO:0003823; F:antigen binding; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Direct protein sequencing; Immunoglobulin V region;
KW   Pyrrolidone carboxylic acid.
FT   DOMAIN        1    112       Ig-like.
FT   MOD_RES       1      1       Pyrrolidone carboxylic acid.
FT   NON_TER     121    121
SQ   SEQUENCE   121 AA;  13566 MW;  480FC53610EF5DAB CRC64;

  Query Match             78.4%;  Score 482;  DB 1;  Length 121;
  Best Local Similarity   76.0%;  Pred. No. 2.5e-44;
  Matches   92;  Conservative   11;  Mismatches   16;  Indels    2;  Gaps    1;

Qy          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSSGMHWVRQAPGKGLEWVAXISYDGSRKYY 60
              ||:||::|||||||||||||| |||||||: |||||||||||||||| | |:||| ||
Db          1 QVKLVQAGGGVVQPGRSLRLSCIASGFTFSNYGMHWVRQAPGKGLEWVAVIWYNGSRTYY 60

Qy         61 ADSVKGRFTISRDNSKNTLYLQMNSLTAXDTAVYYCAK--GVTGSPTLDYWGQGTLVTVS 118
              |||||||||||||| |||::|||   ||||||||:   :  : : |||||| |||||
Db         61 GDSVKGRFTISRDNSKRTLYMZMNSLRTEDTAVYYCARDPDILTAFSFDYWGQGVLVTVS 120

Qy        119 S 119
              |
Db        121 S 121


RESULT 9
Q9UL71
ID   Q9UL71      PRELIMINARY;      PRT;   121 AA.
AC   Q9UL71;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Myosin-reactive immunoglobulin heavy chain variable region
DE   (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
RA   Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA   Young D.C.;
RT   "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT   fetus.";
RL   Clin. Immunol. Immunopathol. 87:184-192(1998).
DR   EMBL; AF035043; AAD56279.1; -.
DR   HSSP; P01852; 1NFD.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
FT   NON_TER       1      1
FT   NON_TER     121    121
SQ   SEQUENCE   121 AA;  13154 MW;  2F045CCFA5D50736 CRC64;

  Query Match             77.1%;  Score 474;  DB 2;  Length 121;
  Best Local Similarity   77.7%;  Pred. No. 1.8e-43;
  Matches   94;  Conservative    5;  Mismatches   20;  Indels    2;  Gaps    1;

Qy          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSSGMHWVRQAPGKGLEWVAXISYDGSRKYY 60
              :|||||||||||||| |||| ||||||||    ||||||||||||||: || ||   ||
Db          1 EVQLVESGGGVVQPGGSLRLFCAASGFTFDGYAMHWVRQAPGKGLEWVSLISGDGGSTYY 60

Qy         61 ADSVKGRFTISRDNSKNTLYLQMNSLTAXDTAVYYCAKG--VTGSPTLDYWGQGTLVTVS 118
              |||||||||||||||:|||||||| | |||:||||||   |      | |||||:||||
Db         61 ADSVKGRFTISRDNSKNSLYLQMNSLRAEDTALYYCAKGKVTTIYDRFDIWGQGTMVTVS 120

Qy        119 S 119
              |
Db        121 S 121


RESULT 10
Q6GMX2
ID   Q6GMX2      PRELIMINARY;      PRT;   493 AA.
AC   Q6GMX2;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Spleen;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
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RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Spleen;
RA   Strausberg R.;
RL   Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC073771; AAH73771.1; -.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 2.
DR   Pfam; PF00047; ig; 3.
DR   SMART; SM00409; IG; 4.
DR   SMART; SM00407; IGc1; 2.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 4.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW   Hypothetical protein.
SQ   SEQUENCE   493 AA;  52865 MW;  55B999305B286203 CRC64;

  Query Match             76.6%;  Score 471;  DB 2;  Length 493;
  Best Local Similarity   76.9%;  Pred. No. 1.9e-42;
  Matches   93;  Conservative    7;  Mismatches   19;  Indels    2;  Gaps    1;

Qy          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSSGMHWVRQAPGKGLEWVAXISYDGSRKYY 60
              :|||||||||:|||| |||||||||| ||| |||||||||| ||: |: ||| | |
Db         20 EVQLVESGGGLVQPGGSLRLSCAASGFIFSSYWMHWVRQAPGKGLVWVSRINSDGSSTSY 79

Qy         61 ADSVKGRFTISRDNSKNTLYLQMNSLTAXDTAVYYCAKGVTGSP--TLDYWGQGTLVTVS 118
              ||||||||||||||:|||||||||||    | ||||||:|     |  ||| |||||:||||
Db         80 ADSVKGRFTISRDNAKNTLYLQMNSLRGEDAAVYYCARGFVSLPRSTLDIWGQGTMVTVS 139

Qy        119 S 119
              |
Db        140 S 140


RESULT 11
Q96BB9
ID   Q96BB9      PRELIMINARY;      PRT;   597 AA.
AC   Q96BB9;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   IGHM protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Primary B-Cells;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Primary B-Cells;
RA   Strausberg R.;
RL   Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC015760; AAH15760.1; -.
DR   PIR; S05271; S05271.
DR   PIR; S24260; S24260.
DR   HSSP; P01861; 1ADQ.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 4.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 5.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_3.
SQ   SEQUENCE   597 AA;  65039 MW;  4FCA3AD8ECE263D9 CRC64;

  Query Match             76.1%;  Score 468;  DB 2;  Length 597;
  Best Local Similarity   75.2%;  Pred. No. 5e-42;
  Matches   94;  Conservative   10;  Mismatches   15;  Indels    6;  Gaps    2;

Qy          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSSGMHWVRQAPGKGLEWVAXISYDGSRKYY 60
              :|||:|||||:|||| |||||||||||:|||  |:|||||||||||: ||  |   ||
Db         20 EVQLLESGGGLVQPGGSLRLSCAASGFSFSSYAMNWVRQAPGKGLEWVSAISGSGGSTYY 79

Qy         61 ADSVKGRFTISRDNSKNTLYLQMNSLTAXDTAVYYCAK-----GVTGSPTL-DYWGQGTL 114
              |||||||||||||::|||||||| | |||||||||       :|: |  |||||||
Db         80 ADSVKGRFTISRDNSRDTLYLQMNSLRAEDTAVYYCAKDPRGYSASGNYTREDYWGQGTL 139

Qy        115 VTVSS 119
              |||||
Db        140 VTVSS 144


RESULT 12
HV3H_HUMAN
ID   HV3H_HUMAN     STANDARD;      PRT;   122 AA.
AC   P01769;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Ig heavy chain V-III region GA.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=74175307; PubMed=4208843;
RA   Florent G., Lehman D., Putnam F.W.;
RT   "The switch point in mu heavy chains of human IgM immunoglobulins.";
RL   Biochemistry 13:2482-2498(1974).
CC   -!- MISCELLANEOUS: This chain was isolated from a Waldenstrom's
CC       macroglobulin.
CC   -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR   PIR; A02052; M3HUGA.
DR   HSSP; P01772; 2FB4.
DR   GO; GO:0005576; C:extracellular; NAS.
DR   GO; GO:0003823; F:antigen binding; NAS.
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DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Direct protein sequencing; Immunoglobulin V region;
KW   Pyrrolidone carboxylic acid.
FT   DOMAIN        1    112       Ig-like.
FT   MOD_RES       1      1       Pyrrolidone carboxylic acid.
FT   NON_TER     122    122
SQ   SEQUENCE   122 AA;  13166 MW;  74E5B6959E84100A CRC64;

  Query Match             76.0%;  Score 467.5;  DB 1;  Length 122;
  Best Local Similarity   68.0%;  Pred. No. 9.3e-43;
  Matches   85;  Conservative   20;  Mismatches   11;  Indels    9;  Gaps    2;

Qy          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSSGMHWVRQAPGKGLEWVAXISYDGSRKYY 60
              ||:||:|||| |:|||||||||||||:||:  |||||||||||:|:: |||:|  :||
Db          1 QVZLVZSGGGAVZPGRSLRLSCAASGFSFSTYAMHWVRQAPGKGLZWLSVISYBGBBZYY 60

Qy         61 ADSVKGRFTISRDNSKNTLYLQMNSLTAXDTAVYYCAK------GVTGSPTLDYWGQGTL 114
              | |||||||||::||:|:||:|||| | :|||||||:       | |:   ||||:|||
Db         61 AASVKGRFTISRBBSKBTMYLEMNSLRAENTAVYYCARSGIALGSVAGT---DYWGZGTL 117

Qy        115 VTVSS 119
              ||:||
Db        118 VTISS 122


RESULT 13
Q6PI81
ID   Q6PI81      PRELIMINARY;      PRT;   478 AA.
AC   Q6PI81;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Primary B-Cells;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Primary B-Cells;
RA   Strausberg R.;
RL   Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC041037; AAH41037.1; -.
DR   HSSP; P01861; 1ADQ.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 3.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 3.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 4.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW   Hypothetical protein.
SQ   SEQUENCE   478 AA;  52666 MW;  17BED38D917970D6 CRC64;

  Query Match             75.9%;  Score 467;  DB 2;  Length 478;
  Best Local Similarity   72.1%;  Pred. No. 5e-42;
  Matches   93;  Conservative    8;  Mismatches   18;  Indels   10;  Gaps    1;

Qy          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSSGMHWVRQAPGKGLEWVAXISYDGSRKYY 60
              :|||||||||:|||| |||||||||||||  | ||||||||||||| |  ||| |||
Db         20 EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYWMSWVRQAPGKGLEWVANIKQDGSEKYY 79

Qy         61 ADSVKGRFTISRDNSKNTLYLQMNSLTAXDTAVYYCAKGVTGSPT----------LDYWG 110
              |||||||||||||:||:|||||||| | ||||||||:    : |          :| ||
Db         80 VDSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCAREFESTMTTVNADYYYFYMDVWG 139

Qy        111 QGTLVTVSS 119
              :|| |||||
Db        140 KGTTVTVSS 148


RESULT 14
Q6PJ95
ID   Q6PJ95      PRELIMINARY;      PRT;   544 AA.
AC   Q6PJ95;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Primary B-Cells;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Primary B-Cells;
RA   Strausberg R.;
RL   Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC019046; AAH19046.1; -.
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DR   HSSP; P01861; 1ADQ.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 3.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 3.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 4.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW   Hypothetical protein.
SQ   SEQUENCE   544 AA;  60102 MW;  1895814B2297C668 CRC64;

  Query Match             75.5%;  Score 464.5;  DB 2;  Length 544;
  Best Local Similarity   76.2%;  Pred. No. 1.1e-41;
  Matches   96;  Conservative    3;  Mismatches   20;  Indels    7;  Gaps    2;

Qy          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSSGMHWVRQAPGKGLEWVAXISYDGSRKYY 60
              | |||||||||||||| |||||||||||  ||: ||||||||||||||||||  ||| | |||
Db         20 QAQLVESGGGVVQPGSSLRLSCAASGFRFSNYGMHWVRQAPGKGLEWVAVFSYDESDKYY 79

Qy         61 ADSVKGRFTISRDNSKNTLYLQMNSLTAXDTAVYYCAKG----VTGS---PTLDYWGQGT 113
              | |||||||||||||||| ||||||   |||||||||      : |      | ||:||
Db         80 AASVKGRFTISRDNSKNTLSLQMNSLRVEDTAVYYCAKDQKPWYSNSWFLTNFDSWGRGT 139

Qy        114 LVTVSS 119
              ||||||
Db        140 LVTVSS 145


RESULT 15
HV3I_HUMAN
ID   HV3I_HUMAN     STANDARD;      PRT;   119 AA.
AC   P01770;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Ig heavy chain V-III region NIE.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=77070269; PubMed=826475;
RA   Ponstingl H., Hilschmann N.;
RT   "The rule of antibody structure. The primary structure of a monoclonal
RT   IgG1 immunoglobulin (myeloma protein Nie). III. The chymotryptic
RT   peptides of the H-chain, alignment of the tryptic peptides and
RT   discussion of the complete structure.";
RL   Hoppe-Seyler's Z. Physiol. Chem. 357:1571-1604(1976).
RN   [2]
RP   DISULFIDE BOND.
RX   MEDLINE=77070267; PubMed=1002129;
RA   Dreker L., Schwarz J., Reichel W., Hilschmann N.;
RT   "Rule of antibody structure. The primary structure of a monoclonal
RT   IgG1 immunoglobulin (myeloma protein Nie), I: purification and
RT   characterization of the protein, the L- and H-chains, the cyanogen
RT   bromide cleavage products, and the disulfide bridges.";
RL   Hoppe-Seyler's Z. Physiol. Chem. 357:1515-1540(1976).
CC   -!- MISCELLANEOUS: This chain was isolated from an IgG1 myeloma
CC       protein.
CC   -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR   PIR; A91668; G1HUNI.
DR   HSSP; P01772; 2FB4.
DR   GO; GO:0005576; C:extracellular; NAS.
DR   GO; GO:0003823; F:antigen binding; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Direct protein sequencing; Immunoglobulin V region;
KW   Pyrrolidone carboxylic acid.
FT   DOMAIN        1    112       Ig-like.
FT   MOD_RES       1      1       Pyrrolidone carboxylic acid.
FT   DISULFID     22     96
FT   NON_TER     119    119
SQ   SEQUENCE   119 AA;  13242 MW;  C96935A6E55E165B CRC64;

  Query Match             75.4%;  Score 464;  DB 1;  Length 119;
  Best Local Similarity   75.6%;  Pred. No. 2.2e-42;
  Matches   90;  Conservative   10;  Mismatches   19;  Indels    0;  Gaps    0;

Qy          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSSGMHWVRQAPGKGLEWVAXISYDGSRKYY 60
              |||||:|||||||||||||||||||||||   :|||||||||||||| :||:|  |:|
Db          1 QVQLVQSGGGVVQPGRSLRLSCAASGFTFSRYTIHWVRQAPGKGLEWVAVMSYBGBBKHY 60

Qy         61 ADSVKGRFTISRDNSKNTLYLQMNSLTAXDTAVYYCAKGVTGSPTLDYWGQGTLVTVSS 119
              |||| |||||||::|||||| ||||   ||||||||:    :    :||||||||||
Db         61 ADSVNGRFTISRNDSKNTLYLNMNSLRPEDTAVYYCARIRDTAMFFAHWGQGTLVTVSS 119


Search completed: October 13, 2005, 03:10:52
Job time : 120.489 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: October 13, 2005, 02:57:16 ; Search time 24.515 Seconds
(without alignments)
467.052 Million cell updates/sec

Title: US-10-010-729A-7
Perfect score: 615
Sequence: 1 QVQLVESGGGVVQPGRSLRL.....VTGSPTLDYWGQGTLVTVSS 119

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	536	87.2	121	2	S19666	Ig heavy chain V r
2	533.5	86.7	120	2	S31112	Ig heavy chain - h
3	533.5	86.7	122	2	S31117	Ig heavy chain - h
4	533	86.7	134	2	S31679	Ig heavy chain V r
5	532	86.5	119	2	F36005	Ig heavy chain V r
6	531	86.3	132	2	S31603	Ig heavy chain V r
7	530.5	86.3	140	2	S70442	Ig heavy chain pre
8	529	86.0	121	2	G36005	Ig heavy chain V r
9	528.5	85.9	118	2	S31116	Ig heavy chain - h
10	527	85.7	130	2	S31601	Ig heavy chain V r
11	527	85.7	135	2	S31598	Ig heavy chain V r
12	524	85.2	111	2	PH1643	Ig heavy chain V r
13	522.5	85.0	114	2	S46390	Ig heavy chain V r
14	521	84.7	133	2	A49028	Ig heavy chain V-I
15	519.5	84.5	139	2	S31674	Ig heavy chain V r
16	516.5	84.0	122	2	E36005	Ig heavy chain V r
17	509.5	82.8	114	2	S46392	Ig heavy chain V r
18	509	82.8	130	2	PL0098	Ig heavy chain pre
19	508.5	82.7	137	2	S31701	Ig heavy chain V r
20	507.5	82.5	128	2	S48797	Ig heavy chain V r
21	507.5	82.5	151	2	A60943	Ig heavy chain pre
22	504	82.0	109	2	PH1644	Ig heavy chain V r
23	502.5	81.7	133	2	S31510	Ig heavy chain - h
24	496	80.7	123	2	S38493	Ig heavy chain - h
25	495.5	80.6	114	2	S46391	Ig heavy chain V r
26	494.5	80.4	136	2	S31587	Ig heavy chain V r
27	493	80.2	109	2	PH1646	Ig heavy chain V r
28	492	80.0	140	2	S31686	Ig heavy chain V r
29	491	79.8	111	2	PH1645	Ig heavy chain V r
30	491	79.8	117	2	S78486	Ig heavy chain V r
31	490	79.7	119	2	S31107	Ig heavy chain - h
32	490	79.7	120	2	S36278	Ig heavy chain V r
33	489.5	79.6	122	1	M3HUAM	Ig heavy chain V-I
34	489.5	79.6	122	2	S69910	Ig V-D-J region (K
35	488	79.3	119	2	S31108	Ig heavy chain - h
36	488	79.3	121	2	I55673	Ig heavy chain - h
37	485.5	78.9	122	2	S31119	Ig heavy chain - h
38	485	78.9	113	2	S38490	Ig heavy chain - h
39	485	78.9	119	2	C36005	Ig heavy chain V r
40	482.5	78.5	147	2	I37780	Ig variable region
41	482	78.4	98	2	PL0116	Ig heavy chain V-I
42	482	78.4	121	1	G1HUHL	Ig heavy chain V-I
43	482	78.4	138	2	B56701	Ig heavy chain V r
44	481	78.2	138	2	S31666	Ig heavy chain V r
45	480.5	78.1	120	2	S44111	Ig heavy chain V-D

ALIGNMENTS

RESULT 1
S19666
Ig heavy chain V region (VH3DJH4) - human
C;Species: Homo sapiens (man)
C;Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 20-Jun-2000
C;Accession: S19666
R;Marks, J.D.; Hoogenboom, H.R.; Bonnert, T.P.; McCafferty, J.; Griffiths, A.D.; Winter,
J. Mol. Biol. 222, 581-597, 1991
A;Title: By-passing immunization. Human antibodies from V-gene libraries displayed on ph
A;Reference number: S19663; MUID:92085276; PMID:1748994
A;Accession: S19666
A;Molecule type: mRNA
A;Residues: 1-121 <MAR>
A;Cross-references: EMBL:X61646; NID:g37688; PIDN:CAA43827.1; PID:g1335369
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 87.2%; Score 536; DB 2; Length 121;
Best Local Similarity 87.0%; Pred. No. 3.5e-43;
Matches 107; Conservative 2; Mismatches 8; Indels 6; Gaps 2;

```
Qy          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSSGMHWVRQAPGKGLEWVAXISYDGSRKYY 60
              |||||:|||||||||||||||||||||||| |||||||||||||||| |||||| |||
Db          1 QVQLVQSGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVISYDGSNKYY 60

Qy         61 ADSVKGRFTISRDNSKNTLYLQMNSLTAXDTAVYYCAKGVTGSPT----LDYWGQGTLVT 116
              |||||||||||||||||||||||| | ||||||||  ||  :    ||||||||||
Db         61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAK--TGYSSGWGYFDYWGQGTLVT 118

Qy        117 VSS 119
              |||
Db        119 VSS 121
```

RESULT 2
S31112
Ig heavy chain - human
C;Species: Homo sapiens (man)
C;Date: 02-Dec-1993 #sequence_revision 26-May-1995 #text_change 17-Mar-1999
C;Accession: S31112
R;Raaphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurman
Eur. J. Immunol. 22, 247-251, 1992
A;Title: Restricted utilization of germ-line V(H)3 genes and short diverse third complem
A;Reference number: S31104; MUID:92111633; PMID:1730252
A;Accession: S31112
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: mRNA
A;Residues: 1-120 <RAA>
A;Cross-references: EMBL:X62961
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1991
C;Superfamily: immunoglobulin V region; immunoglobulin homology

```
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

  Query Match             86.7%;  Score 533.5;  DB 2;  Length 120;
  Best Local Similarity   88.3%;  Pred. No. 5.9e-43;
  Matches  106;  Conservative    0;  Mismatches   13;  Indels    1;  Gaps    1;

Qy          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSSGMHWVRQAPGKGLEWVAXISYDGSRKYY 60
              ||||||||||||||||||||||||||||||  ||||||||||||||| |||||| |||
Db          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYY 60

Qy         61 ADSVKGRFTISRDNSKNTLYLQMNSLTAXDTAVYYCAKG-VTGSPTLDYWGQGTLVTVSS 119
              |||||||||||||||||||||||| | ||||||| | |      ||||||||||||
Db         61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCATGVVVVVAATDYWGQGTLVTVSS 120


RESULT 3
S31117
Ig heavy chain - human
C;Species: Homo sapiens (man)
C;Date: 02-Dec-1993 #sequence_revision 26-May-1995 #text_change 17-Mar-1999
C;Accession: S31117
R;Raaphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurman
Eur. J. Immunol. 22, 247-251, 1992
A;Title: Restricted utilization of germ-line V(H)3 genes and short diverse third complem
A;Reference number: S31104; MUID:92111633; PMID:1730252
A;Accession: S31117
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: mRNA
A;Residues: 1-122 <RAA>
A;Cross-references: EMBL:X62967
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1991
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

  Query Match             86.7%;  Score 533.5;  DB 2;  Length 122;
  Best Local Similarity   86.1%;  Pred. No. 6e-43;
  Matches  105;  Conservative    1;  Mismatches   13;  Indels    3;  Gaps    1;

Qy          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSSGMHWVRQAPGKGLEWVAXISYDGSRKYY 60
              ||||||||||||||||||||||||||||||  ||||||||||||||| | |||| |||
Db          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVIWYDGSNKYY 60

Qy         61 ADSVKGRFTISRDNSKNTLYLQMNSLTAXDTAVYYCAKGVTGSPT---LDYWGQGTLVTV 117
              ||||||||||||||||||||||||| | ||||||||:     |     ||||||||||
Db         61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDFFAPPNWSHFDYWGQGTLVTV 120

Qy        118 SS 119
              ||
Db        121 SS 122


RESULT 4
S31679
Ig heavy chain V region - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Accession: S31679
R;Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.
submitted to the EMBL Data Library, June 1992
A;Description: Mechanisms that generate human immunoglobulin diversity operate from the
A;Reference number: S31585
A;Accession: S31679
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-134 <CUI>
A;Cross-references: EMBL:Z14203; NID:g30965; PIDN:CAA78572.1; PID:g30966
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;34-117/Domain: immunoglobulin homology <IMM>

  Query Match             86.7%;  Score 533;  DB 2;  Length 134;
  Best Local Similarity   88.2%;  Pred. No. 7.3e-43;
  Matches  105;  Conservative    1;  Mismatches    9;  Indels    4;  Gaps    1;

Qy          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSSGMHWVRQAPGKGLEWVAXISYDGSRKYY 60
              ||||||||||||||||||||||||||||||  ||||||||||||||| |||||| |||
Db         20 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYY 79

Qy         61 ADSVKGRFTISRDNSKNTLYLQMNSLTAXDTAVYYCAKGVTGSPTLDYWGQGTLVTVSS 119
              ||||||||||||||||||||||| | ||||||||:   |    ||||||||||||
Db         80 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARESRG----DYWGQGTLVTVSS 134


RESULT 5
F36005
Ig heavy chain V region (M49) - human
C;Species: Homo sapiens (man)
C;Date: 21-Dec-1990 #sequence_revision 21-Dec-1990 #text_change 09-Jul-2004
C;Accession: F36005
R;Schroeder Jr., H.W.; Wang, J.Y.
Proc. Natl. Acad. Sci. U.S.A. 87, 6146-6150, 1990
A;Title: Preferential utilization of conserved immunoglobulin heavy chain variable gene
A;Reference number: A36005; MUID:90349571; PMID:2117273
A;Accession: F36005
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-119 <SCH>
A;Cross-references: UNIPROT:Q8WUK1; GB:M34026
C;Genetics:
A;Gene: GDB:IGH@; IGHDY1
A;Cross-references: GDB:118731; OMIM:146910
A;Map position: 14q32.33-14q32.33
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

  Query Match             86.5%;  Score 532;  DB 2;  Length 119;
  Best Local Similarity   86.6%;  Pred. No. 8e-43;
  Matches  103;  Conservative    2;  Mismatches   14;  Indels    0;  Gaps    0;

Qy          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSSGMHWVRQAPGKGLEWVAXISYDGSRKYY 60
              ||||||||||||||||||||||||||||||  ||||||||||||||| |||||| |||
Db          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYY 60

Qy         61 ADSVKGRFTISRDNSKNTLYLQMNSLTAXDTAVYYCAKGVTGSPTLDYWGQGTLVTVSS 119
              ||||||||||||||||||||||| | ||||||||:    |   | |||||:|||||
Db         61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDRKASDAFDIWGQGTMVTVSS 119


RESULT 6
S31603
Ig heavy chain V region - human
C;Species: Homo sapiens (man)
C;Date: 03-Mar-1994 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Accession: S31603
R;Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.
submitted to the EMBL Data Library, June 1992
A;Description: Mechanisms that generate human immunoglobulin diversity operate from the
A;Reference number: S31585
A;Accession: S31603
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-132 <CUI>
A;Cross-references: EMBL:Z14168; NID:g30999; PIDN:CAA78537.1; PID:g31000
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;30-113/Domain: immunoglobulin homology <IMM>

  Query Match             86.3%;  Score 531;  DB 2;  Length 132;
  Best Local Similarity   88.2%;  Pred. No. 1.1e-42;
  Matches  105;  Conservative    1;  Mismatches   11;  Indels    2;  Gaps    1;

Qy          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSSGMHWVRQAPGKGLEWVAXISYDGSRKYY 60
              ||||||||||||||||||||||||||||||  ||||||||||||||| |||||| |||
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Db         16 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVISYDGSNKYY 75

Qy         61 ADSVKGRFTISRDNSKNTLYLQMNSLTAXDTAVYYCAKGVTGSPTLDYWGQGTLVTVSS 119
              ||||||||||||||||||||||| | | |||||||||  :      ||||||||||||
Db         76 ADSVKGRFTISRDNSKNTLYLQMNGLRAEDTAVYYCAKDL--FYYFDYWGQGTLVTVSS 132


RESULT 7
S70442
Ig heavy chain precursor V region (mu) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 09-Jul-2004
C;Accession: S70442
R;Cuisinier, A.M.; Fumoux, F.; Fougereau, M.; Tonnelle, C.
Mol. Immunol. 29, 1363-1373, 1992
A;Title: IgM kappa/lambda EBV human B cell clone: an early step of differentiation of fe
A;Reference number: S70442; MUID:93024508; PMID:1383695
A;Accession: S70442
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-140 <CUI>
A;Cross-references: UNIPROT:Q8WUK1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;34-117/Domain: immunoglobulin homology <IMM>

  Query Match             86.3%;  Score 530.5;  DB 2;  Length 140;
  Best Local Similarity   85.8%;  Pred. No. 1.3e-42;
  Matches  103;  Conservative    4;  Mismatches   12;  Indels    1;  Gaps    1;

Qy          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSSGMHWVRQAPGKGLEWVAXISYDGSRKYY 60
              |||||||||||||| |||||||||||: |||||||||||||||| | |||| |||
Db         20 QVQLVESGGGVVQPGGSLRLSCAASGFTFSNYGMHWVRQAPGKGLEWVAFIRYDGSNKYY 79

Qy         61 ADSVKGRFTISRDNSKNTLYLQMNSLTAXDTAVYYCAKG-VTGSPTLDYWGQGTLVTVSS 119
              |||||||||||||||||||||||| | ||||||||:  : |:   ||||||||||||
Db         80 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDHIVGATYFDYWGQGTLVTVSS 139


RESULT 8
G36005
Ig heavy chain V region (M74) - human
C;Species: Homo sapiens (man)
C;Date: 21-Dec-1990 #sequence_revision 21-Dec-1990 #text_change 09-Jul-2004
C;Accession: G36005
R;Schroeder Jr., H.W.; Wang, J.Y.
Proc. Natl. Acad. Sci. U.S.A. 87, 6146-6150, 1990
A;Title: Preferential utilization of conserved immunoglobulin heavy chain variable gene
A;Reference number: A36005; MUID:90349571; PMID:2117273
A;Accession: G36005
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-121 <SCH>
A;Cross-references: UNIPROT:Q8WUK1; GB:M34031
C;Genetics:
A;Gene: GDB:IGH@; IGHDY1
A;Cross-references: GDB:118731; OMIM:146910
A;Map position: 14q32.33-14q32.33
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

  Query Match             86.0%;  Score 529;  DB 2;  Length 121;
  Best Local Similarity   86.8%;  Pred. No. 1.6e-42;
  Matches  105;  Conservative    1;  Mismatches   13;  Indels    2;  Gaps    1;

Qy          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSSGMHWVRQAPGKGLEWVAXISYDGSRKYY 60
              ||||||||||||||||||||||||||||||  |||||||||||||||| |||||| |||
Db          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYY 60

Qy         61 ADSVKGRFTISRDNSKNTLYLQMNSLTAXDTAVYYCAKGVT--GSPTLDYWGQGTLVTVS 118
              ||||||||||||||||||||||| | ||||||||:     |    ||||||||||||
Db         61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDRKDWGWALFDYWGQGTLVTVS 120

Qy        119 S 119
              |
Db        121 S 121


RESULT 9
S31116
Ig heavy chain - human
C;Species: Homo sapiens (man)
C;Date: 02-Dec-1993 #sequence_revision 26-May-1995 #text_change 09-Jul-2004
C;Accession: S31116
R;Raaphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurma
Eur. J. Immunol. 22, 247-251, 1992
A;Title: Restricted utilization of germ-line V(H)3 genes and short diverse third comple
A;Reference number: S31104; MUID:92111633; PMID:1730252
A;Accession: S31116
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: mRNA
A;Residues: 1-118 <RAA>
A;Cross-references: UNIPROT:Q8WUK1; EMBL:X62966
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1991
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

  Query Match             85.9%;  Score 528.5;  DB 2;  Length 118;
  Best Local Similarity   87.4%;  Pred. No. 1.7e-42;
  Matches  104;  Conservative    1;  Mismatches   13;  Indels    1;  Gaps    1;

Qy          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSSGMHWVRQAPGKGLEWVAXISYDGSRKYY 60
              |||||||||||||||||||||||||||||| |||||||||||||| |||||| |||
Db          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVISYDGSNKYY 60

Qy         61 ADSVKGRFTISRDNSKNTLYLQMNSLTAXDTAVYYCAKGVTGSPTLDYWGQGTLVTVSS 119
              |||||||||||||||||||||||| | ||||||||    |    | |||||:|||||
Db         61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCATD-GGKAAPDIWGQGTMVTVSS 118


RESULT 10
S31601
Ig heavy chain V region - human
C;Species: Homo sapiens (man)
C;Date: 03-Mar-1994 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Accession: S31601
R;Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.
submitted to the EMBL Data Library, June 1992
A;Description: Mechanisms that generate human immunoglobulin diversity operate from the
A;Reference number: S31585
A;Accession: S31601
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-130 <CUI>
A;Cross-references: EMBL:Z14192; NID:g31018; PIDN:CAA78561.1; PID:g31019
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;30-113/Domain: immunoglobulin homology <IMM>

  Query Match             85.7%;  Score 527;  DB 2;  Length 130;
  Best Local Similarity   87.4%;  Pred. No. 2.6e-42;
  Matches  104;  Conservative    2;  Mismatches    9;  Indels    4;  Gaps    1;

Qy          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSSGMHWVRQAPGKGLEWVAXISYDGSRKYY 60
              |||||||||||||||||||||||||||||| |||||||||||||| | |||| |||
Db         16 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVIWYDGSNKYY 75

Qy         61 ADSVKGRFTISRDNSKNTLYLQMNSLTAXDTAVYYCAKGVTGSPTLDYWGQGTLVTVSS 119
              | ||||||||||||||||||| | ||||||||:|:      ||||||||||||
Db         76 AVSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARGL----GFDYWGQGTLVTVSS 130


RESULT 11
S31598
Ig heavy chain V region - human
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C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Accession: S31598
R;Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.
submitted to the EMBL Data Library, June 1992
A;Description: Mechanisms that generate human immunoglobulin diversity operate from the
A;Reference number: S31585
A;Accession: S31598
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-135 <CUI>
A;Cross-references: EMBL:Z14170; NID:g31001; PIDN:CAA78539.1; PID:g31002
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;31-114/Domain: immunoglobulin homology <IMM>

  Query Match             85.7%;  Score 527;  DB 2;  Length 135;
  Best Local Similarity   87.4%;  Pred. No. 2.7e-42;
  Matches  104;  Conservative    0;  Mismatches   15;  Indels    0;  Gaps    0;

Qy          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSSGMHWVRQAPGKGLEWVAXISYDGSRKYY 60
              |||||||||||||||| |||||||||||||||| |||||||||||||||| | |||| |||
Db         17 QVQLVESGGGVVQPGGSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAFIRYDGSNKYY 76

Qy         61 ADSVKGRFTISRDNSKNTLYLQMNSLTAXDTAVYYCAKGVTGSPTLDYWGQGTLVTVSS 119
              ||||||||||||||||||||||||| | |||||||||          ||||||||||||
Db         77 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKISWEVSRFDYWGQGTLVTVSS 135


RESULT 12
PH1643
Ig heavy chain V region (clone 6H7) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 09-Jul-2004
C;Accession: PH1643
R;Hillson, J.L.; Karr, N.S.; Oppliger, I.R.; Mannik, M.; Sasso, E.H.
J. Exp. Med. 178, 331-336, 1993
A;Title: The structural basis of germline-encoded VH3 immunoglobulin binding to staphylc
A;Reference number: PH1642; MUID:93301610; PMID:8315388
A;Accession: PH1643
A;Molecule type: mRNA
A;Residues: 1-111 <HIL>
A;Cross-references: UNIPROT:Q8WUK1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;7-90/Domain: immunoglobulin homology <IMM>

  Query Match             85.2%;  Score 524;  DB 2;  Length 111;
  Best Local Similarity   91.0%;  Pred. No. 4.2e-42;
  Matches  101;  Conservative    0;  Mismatches   10;  Indels    0;  Gaps    0;

Qy          9 GGVVQPGRSLRLSCAASGFTFSSSGMHWVRQAPGKGLEWVAXISYDGSRKYYADSVKGRF 68
              |||||||||||||||||||||||| |||||||||||||||| |||||| ||||||||||
Db          1 GGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVISYDGSNKYYADSVKGRF 60

Qy         69 TISRDNSKNTLYLQMNSLTAXDTAVYYCAKGVTGSPTLDYWGQGTLVTVSS 119
              |||||||||||||||| | |||||||||    ||  ||||||||||||||
Db         61 TISRDNSKNTLYLQMNSLRAEDTAVYYCAKDPLGSRALDYWGQGTLVTVSS 111


RESULT 13
S46390
Ig heavy chain V region - human
C;Species: Homo sapiens (man)
C;Date: 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change 20-Jun-2000
C;Accession: S46390
R;Figini, M.; Marks, J.D.; Winter, G.; Griffiths, A.D.
J. Mol. Biol. 239, 68-78, 1994
A;Title: In vitro assembly of repertoires of antibody chains on the surface of phage by
A;Reference number: S46390; MUID:94254092; PMID:8196048
A;Accession: S46390
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-114 <FIG>
A;Cross-references: EMBL:Z31686; NID:g509782; PIDN:CAA83491.1; PID:g1335143
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

  Query Match             85.0%;  Score 522.5;  DB 2;  Length 114;
  Best Local Similarity   86.6%;  Pred. No. 5.9e-42;
  Matches  103;  Conservative    2;  Mismatches    9;  Indels    5;  Gaps    1;

Qy          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSSGMHWVRQAPGKGLEWVAXISYDGSRKYY 60
              :|||||||||||||||||||||||||||||||  |||||||||||||||| |||||| |||
Db          1 EVQLVESGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYY 60

Qy         61 ADSVKGRFTISRDNSKNTLYLQMNSLTAXDTAVYYCAKGVTGSPTLDYWGQGTLVTVSS 119
              |||||||||||||||||||||||| | ||||||||:          ||||||||||||
Db         61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDWG-----DYWGQGTLVTVSS 114


RESULT 14
A49028
Ig heavy chain V-III region - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 21-Jan-1994 #sequence_revision 18-Nov-1994 #text_change 23-Jul-1999
C;Accession: A49028
R;Timmers, E.; Kenter, M.; Thompson, A.; Kraakman, M.E.; Berman, J.E.; Alt, F.W.; Schuur,
Eur. J. Immunol. 21, 2355-2363, 1991
A;Title: Diversity of immunoglobulin heavy chain gene segment rearrangement in B lymphob
A;Reference number: A49028; MUID:92008140; PMID:1915549
A;Accession: A49028
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-133 <TIM>
A;Cross-references: GB:S64471; NID:g236904; PIDN:AAB20011.1; PID:g236905
A;Experimental source: X-linked agammaglobulinemia patients, B lymphoblastoid cell lines
A;Note: sequence extracted from NCBI backbone (NCBIN:64471, NCBIP:64470)
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

  Query Match             84.7%;  Score 521;  DB 2;  Length 133;
  Best Local Similarity   82.9%;  Pred. No. 9.6e-42;
  Matches  102;  Conservative    3;  Mismatches   14;  Indels    4;  Gaps    1;

Qy          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSSGMHWVRQAPGKGLEWVAXISYDGSRKYY 60
              |||||||||||||||||||||||||||||||| ||||| |||||||||| | |||| |||
Db          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVLQAPGKGLEWVAVIWYDGSNKYY 60

Qy         61 ADSVKGRFTISRDNSKNTLYLQMNSLTAXDTAVYYCAKG----VTGSPTLDYWGQGTLVT 116
              |||||||||||||||||||||||| | ||||||||:    : :   ||||||||  |
Db         61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDRRLTIAAAGNFDYWGQGTLAT 120

Qy        117 VSS 119
              |||
Db        121 VSS 123


RESULT 15
S31674
Ig heavy chain V region - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Accession: S31674
R;Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.
submitted to the EMBL Data Library, June 1992
A;Description: Mechanisms that generate human immunoglobulin diversity operate from the
A;Reference number: S31585
A;Accession: S31674
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-139 <CUI>
A;Cross-references: EMBL:Z14204; NID:g30967; PIDN:CAA78573.1; PID:g30968
C;Superfamily: immunoglobulin V region; immunoglobulin homology
```

C;Keywords: heterotetramer; immunoglobulin
F;34-117/Domain: immunoglobulin homology <IMM>

Query Match 84.5%; Score 519.5; DB 2; Length 139;
Best Local Similarity 87.5%; Pred. No. 1.4e-41;
Matches 105; Conservative 1; Mismatches 13; Indels 1; Gaps 1;

```
Qy          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSSGMHWVRQAPGKGLEWVAXISYDGSRKYY 60
              |||||||||||||||||||||||||||||| ||||||||| ||||||| |||||| |||
Db         20 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPCKGLEWVAVISYDGSNKYY 79

Qy         61 ADSVKGRFTISRDNSKNTLYLQMNSLTAXDTAVYYCAK-GVTGSPTLDYWGQGTLVTVSS 119
              |||||||||||||||||||||||| | ||||||||| |:      | ||||||||||
Db         80 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKAGLGFFNWFDPWGQGTLVTVSS 139
```

Search completed: October 13, 2005, 03:11:46
Job time : 25.515 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: October 13, 2005, 02:44:40 ; Search time 122.575 Seconds
(without alignments)
375.480 Million cell updates/sec

Title: US-10-010-729A-7
Perfect score: 615
Sequence: 1 QVQLVESGGGVVQPGRSLRL.....VTGSPTLDYWGQGTLVTVSS 119

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	611	99.3	119	5	ABB07169	Abb07169 sHigM22 h
2	611	99.3	119	5	ABB07186	Abb07186 sHigM22 h
3	611	99.3	119	8	ADI26654	Adi26654 Human ant
4	544	88.5	123	6	ABR55789	Abr55789 Heavy cha
5	542.5	88.2	254	3	AAY56287	Aay56287 HCAT1 clo
6	542.5	88.2	490	3	AAY56637	Aay56637 hCAT1 bin
7	540.5	87.9	120	6	ADA89174	Ada89174 Human ant
8	540.5	87.9	121	8	ADP47108	Adp47108 Human pho
9	540	87.8	121	8	ADP22284	Adp22284 Human ant
10	539	87.6	119	6	AAE32095	Aae32095 Human VEG
11	538.5	87.6	118	5	ABG30463	Abg30463 Human ant
12	538.5	87.6	241	7	ADG30467	Adg30467 Human GMB
13	538	87.5	117	8	ADO36354	Ado36354 Intracell
14	538	87.5	119	7	ADL91327	Adl91327 VH chain
15	537.5	87.4	583	8	ABM82698	Abm82698 Human dia
16	537	87.3	117	8	ADI22094	Adi22094 Anti-plat
17	537	87.3	121	8	ADP22186	Adp22186 Human ant
18	535.5	87.1	223	2	AAY08598	Aay08598 Anti-huma
19	535	87.0	117	8	ADI22096	Adi22096 Anti-plat
20	535	87.0	244	7	ADG30422	Adg30422 Human GMB
21	535	87.0	519	5	AAU81993	Aau81993 Human sec
22	534.5	86.9	118	6	AAE32097	Aae32097 Human VEG
23	534	86.8	117	8	ADI22095	Adi22095 Anti-plat
24	534	86.8	117	8	ADO36345	Ado36345 Intracell
25	534	86.8	119	7	ADL91318	Adl91318 VH chain
26	532.5	86.6	121	8	ADP47227	Adp47227 Human pho
27	532.5	86.6	223	8	ADL70773	Adl70773 Anti-TNFa
28	532	86.5	119	4	AAU02515	Aau02515 Anti-adip
29	531.5	86.4	116	7	ADC60976	Adc60976 Human ant
30	531.5	86.4	135	7	ADC61032	Adc61032 Human ant
31	531	86.3	119	2	AAR95216	Aar95216 Human foe
32	530.5	86.3	126	7	ADP03963	Adp03963 Murine-ex
33	530.5	86.3	252	5	ABP45616	Abp45616 Human BLy
34	530.5	86.3	252	7	ADG96443	Adg96443 Single ch
35	530	86.2	123	8	ADR72700	Adr72700 Human mon
36	530	86.2	123	8	ADR72704	Adr72704 Human mon
37	530	86.2	123	8	ADR72698	Adr72698 Human mon
38	530	86.2	124	8	ADP46956	Adp46956 Murine he
39	530	86.2	472	8	ADR72764	Adr72764 Human mon
40	529.5	86.1	121	8	ADP47221	Adp47221 Human pho
41	529.5	86.1	252	5	ABP45508	Abp45508 Human BLy
42	529.5	86.1	252	7	ADG96335	Adg96335 Single ch
43	529	86.0	115	3	AAB39519	Aab39519 Anti-IL12
44	528.5	85.9	249	5	ABP44501	Abp44501 Human BLy
45	528.5	85.9	249	7	ADG95328	Adg95328 Single ch

ALIGNMENTS

RESULT 1
ABB07169
ID ABB07169 standard; protein; 119 AA.
XX
AC ABB07169;
XX
DT 13-MAR-2002 (first entry)
XX
DE sHigM22 heavy chain variable region clone A sequence.
XX
KW Neuromodulatory; central nervous system; CNS; sHIgM22; LYM 22; AKJR4;
KW ebvHigM MsI19D10; ebv HIgM CB2bG8; CB2iE12; CB2iE7; MSI19E5; virucide;
KW antiparkinsonian; neuroprotective; nootropic; vulnerary.
XX
OS Homo sapiens.
XX
PN WO200185797-A1.
XX
PD 15-NOV-2001.
XX
PF 30-MAY-2000; 2000WO-US014902.
XX
PR 10-MAY-2000; 2000US-00568351.
XX
PA (MAYO-) MAYO FOUND MEDICAL EDUCATION RES.
XX
PI Rodriguez M, Miller DJ, Pease LR;
XX
DR WPI; 2002-066596/09.
DR N-PSDB; ABA94216.
XX
PT Novel neuromodulatory agent (a human IgM monoclonal antibody), promoting
PT neurite outgrowth, regeneration, remyelination and neuroprotection in
PT central nervous system, useful to treat post-infectious
PT encephalomyelitis.
XX
PS Claim 23; Fig 17; 219pp; English.
XX
CC The invention provides a neuromodulatory agent (I) capable of promoting
CC neurite outgrowth, regeneration, remyelination and neuroprotection in
CC central nervous system (CNS). (I) is capable of inducing remyelination,
CC promoting cellular proliferation of glial cells, and promoting Ca2+
CC signaling with oligodendrocytes. An humanised antibody to (I) can be
CC selected from antibody sHIgM22 (LYM 22), ebvHigM MsI19D10, ebv HIgM
CC CB2bG8, AKJR4, CB2iE12, CB2iE7 or MSI19E5. (I) is useful for stimulating
CC remyelination of CNS axons, stimulating proliferation of glial cells in
CC CNS axons, or treating demyelinating disease of CNS in a mammal in need
CC of such therapy. (I) is capable of binding to structures and cells within

```
CC   CNS. (I) is preferably useful for treating a demyelinating disease of CNS
CC   of a mouse infected with Strain DA of Theiler's murine encephalomyelitis
CC   (TMEV) or for treating a human being having multiple sclerosis, or a
CC   human or domestic animal with a viral demyelinating disease, or a post-
CC   neural disease of CNS. (I) is also useful for an in vitro method of
CC   stimulating the proliferation of glial cells from mixed cell culture. (I)
CC   is also useful for stimulating remyelination of CNS axons. The antibodies
CC   are useful for preventing infection by a bacterium, virus or like
CC   pathogen that causes demyelination or other neurodegenerative condition
CC   in a subject. Methods where (I) is administered to a patient are useful
CC   for treating multiple sclerosis, Parkinson's disease, Alzheimer's
CC   disease, amyotrophic lateral sclerosis (ALS), a viral demyelinating
CC   disease, CNS diseases, and other conditions in the CNS where nerves are
CC   damaged as by trauma. The present sequence represents the sHigM22 heavy
CC   chain variable region clone A amino acid sequence
XX
SQ   Sequence 119 AA;

  Query Match             99.3%;  Score 611;  DB 5;  Length 119;
  Best Local Similarity   98.3%;  Pred. No. 2.7e-49;
  Matches  117;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSSGMHWVRQAPGKGLEWVAXISYDGSRKYY 60
              |||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Db          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSSGMHWVRQAPGKGLEWVAVISYDGSRKYY 60

Qy         61 ADSVKGRFTISRDNSKNTLYLQMNSLTAXDTAVYYCAKGVTGSPTLDYWGQGTLVTVSS 119
              |||||||||||||||||||||||||| |||||||||||||||||||||||||||||||||
Db         61 ADSVKGRFTISRDNSKNTLYLQMNSLTADDTAVYYCAKGVTGSPTLDYWGQGTLVTVSS 119


RESULT 2
ABB07186
ID   ABB07186 standard; protein; 119 AA.
XX
AC   ABB07186;
XX
DT   13-MAR-2002  (first entry)
XX
DE   sHigM22 heavy chain variable region clone B sequence.
XX
KW   Neuromodulatory; central nervous system; CNS; sHIgM22; LYM 22; AKJR4;
KW   ebvHigM MsI19D10; ebv HIgM CB2bG8; CB2iE12; CB2iE7; MSI19E5; virucide;
KW   antiparkinsonian; neuroprotective; nootropic; vulnerary.
XX
OS   Homo sapiens.
XX
PN   WO200185797-A1.
XX
PD   15-NOV-2001.
XX
PF   30-MAY-2000; 2000WO-US014902.
XX
PR   10-MAY-2000; 2000US-00568351.
XX
PA   (MAYO-) MAYO FOUND MEDICAL EDUCATION RES.
XX
PI   Rodriguez M,  Miller DJ,  Pease LR;
XX
DR   WPI; 2002-066596/09.
DR   N-PSDB; ABA94243.
XX
PT   Novel neuromodulatory agent (a human IgM monoclonal antibody), promoting
PT   neurite outgrowth, regeneration, remyelination and neuroprotection in
PT   central nervous system, useful to treat post-infectious
PT   encephalomyelitis.
XX
PS   Claim 23; Fig 17; 219pp; English.
XX
CC   The invention provides a neuromodulatory agent (I) capable of promoting
CC   neurite outgrowth, regeneration, remyelination and neuroprotection in
CC   central nervous system (CNS). (I) is capable of inducing remyelination,
CC   promoting cellular proliferation of glial cells, and promoting Ca2+
CC   signaling with oligodendrocytes. An humanised antibody to (I) can be
CC   selected from antibody sHIgM22 (LYM 22), ebvHigM MsI19D10, ebv HIgM
CC   CB2bG8, AKJR4, CB2iE12, CB2iE7 or MSI19E5. (I) is useful for stimulating
CC   remyelination of CNS axons, stimulating proliferation of glial cells in
CC   CNS axons, or treating demyelinating disease of CNS in a mammal in need
CC   of such therapy. (I) is capable of binding to structures and cells within
CC   CNS. (I) is preferably useful for treating a demyelinating disease of CNS
CC   of a mouse infected with Strain DA of Theiler's murine encephalomyelitis
CC   (TMEV) or for treating a human being having multiple sclerosis, or a
CC   human or domestic animal with a viral demyelinating disease, or a post-
CC   neural disease of CNS. (I) is also useful for an in vitro method of
CC   stimulating the proliferation of glial cells from mixed cell culture. (I)
CC   is also useful for stimulating remyelination of CNS axons. The antibodies
CC   are useful for preventing infection by a bacterium, virus or like
CC   pathogen that causes demyelination or other neurodegenerative condition
CC   in a subject. Methods where (I) is administered to a patient are useful
CC   for treating multiple sclerosis, Parkinson's disease, Alzheimer's
CC   disease, amyotrophic lateral sclerosis (ALS), a viral demyelinating
CC   disease, CNS diseases, and other conditions in the CNS where nerves are
CC   damaged as by trauma. The present sequence represents the sHigM22 heavy
CC   chain variable region clone B amino acid sequence
XX
SQ   Sequence 119 AA;

  Query Match             99.3%;  Score 611;  DB 5;  Length 119;
  Best Local Similarity   98.3%;  Pred. No. 2.7e-49;
  Matches  117;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSSGMHWVRQAPGKGLEWVAXISYDGSRKYY 60
              |||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Db          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSSGMHWVRQAPGKGLEWVAIISYDGSRKYY 60

Qy         61 ADSVKGRFTISRDNSKNTLYLQMNSLTAXDTAVYYCAKGVTGSPTLDYWGQGTLVTVSS 119
              |||||||||||||||||||||||||| |||||||||||||||||||||||||||||||||
Db         61 ADSVKGRFTISRDNSKNTLYLQMNSLTAEDTAVYYCAKGVTGSPTLDYWGQGTLVTVSS 119


RESULT 3
ADI26654
ID   ADI26654 standard; protein; 119 AA.
XX
AC   ADI26654;
XX
DT   15-APR-2004  (first entry)
XX
DE   Human anti IgM antibody sHIgM22 VH protein.
XX
KW   Human; antibody; IgM; remyelination; neuronal growth; autoantibody;
KW   demyelination disease; multiple sclerosis; central nervous system; CNS;
KW   axon; glial cell proliferation;
KW   Theiler's murine encephalomyelitis virus infection; CNS injury;
KW   spinal cord injury.
XX
OS   Homo sapiens.
XX
PN   US2003185827-A1.
XX
PD   02-OCT-2003.
XX
PF   13-NOV-2001; 2001US-00010729.
XX
PR   29-APR-1994;   94US-00236520.
PR   08-AUG-1996;   96US-00692084.
PR   07-JAN-1997;   97US-00779784.
PR   28-MAY-1999;   99US-00322862.
PR   30-MAY-2000; 2000US-00580787.
PR   05-DEC-2000; 2000US-00730473.
XX
PA   (MAYO-) MAYO FOUND.
XX
PI   Rodriguez M,  Miller DJ,  Pease LR;
XX
DR   WPI; 2004-119219/12.
```

DR N-PSDB; ADI26655.
XX
PT New human immunoglobulin M antibody for treating or preventing a
PT demyelinating disease of the central nervous system in a human or
PT domestic animal, such as multiple sclerosis.
XX
PS Claim 7; Fig 35; 159pp; English.
XX
CC The invention relates to an antibody (I) produced by injecting an
CC immunocompetent host with an antibody peptide, and harvesting the
CC antibody, where the peptide comprises a human anti-IgM antibody fragment
CC given in the specification, or active fragments. Also included are
CC stimulating remyelination of central nervous system (CNS) axons in a
CC mammal (comprising administering a monoclonal antibody, or mixtures,
CC monomers, active fragments, or recombinant antibodies derived from it,
CC characterised by their ability to bind structures and cells within the
CC CNS, including oligodendrocytes), stimulating the proliferation of glial
CC cells in CNS axons in a mammal (comprising administering a monoclonal
CC antibody, or mixtures, monomers, active fragments, or recombinant
CC antibodies derived from it, characterised by their ability to bind
CC structures and cells within the CNS), treating or preventing a
CC demyelinating disease of the CNS in a mammal (comprising administering a
CC monoclonal antibody, or mixtures, monomers, active fragments, or
CC recombinant antibodies derived from it, characterised by their ability to
CC bind structures and cells within the CNS, and to stimulate remyelination
CC of axons of the CNS), stimulating, in vitro, the proliferation of glial
CC cells from mixed cell culture, stimulating remyelination of CNS axons in
CC a mammal, a DNA sequence (or degenerate variant of it) which encodes an
CC antibody(or a peptide analogue, hapten, or active fragment of it, where
CC the DNA sequence consists of a sequence encoding an anti IgM antibody), a
CC probe capable of screening for the antibody, an assay for screening drugs
CC and other agents for the ability to modulate the production or mimic the
CC activities of mAB sHIgM22, sHIgM46, or combinations of them, a
CC recombinant virus transformed with recombinant antibody nucleic acids or
CC vector, imaging a portion of the CNS using the antibody and diagnosing or
CC monitoring demyelination and/or remyelination of the CNS comprising using
CC CNS image. The antibody is used to stimulate remyelination of CNS axons,
CC and to stimulate the proliferation of glial cells in CNS axons,
CC optionally in vitro. The antibody is used to treat or prevent a
CC demyelinating disease of the CNS in a human or domestic animal, such as
CC multiple sclerosis, or a disease, other injury or dysfunction of the CNS,
CC preferably the mammal is a mouse infected with Strain DA of Theiler's
CC murine encephalomyelitis virus. The antibody is used to treat a spinal
CC cord injury and used to screen drugs and other agents for the ability to
CC modulate the production or mimic the activities of the antibody. The
CC antibody can be used to image a portion of the CNS which can be used to
CC diagnose or monitor demyelination and/or remyelination of the CNS. The
CC present sequence is a variable region of a human anti-IgM antibody (or
CC fragment).
XX
SQ Sequence 119 AA;

Query Match 99.3%; Score 611; DB 8; Length 119;
Best Local Similarity 99.2%; Pred. No. 2.7e-49;
Matches 118; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSSGMHWVRQAPGKGLEWVAXISYDGSRKYY 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Db          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSSGMHWVRQAPGKGLEWVAVISYDGSRKYY 60

Qy         61 ADSVKGRFTISRDNSKNTLYLQMNSLTAXDTAVYYCAKGVTGSPTLDYWGQGTLVTVSS 119
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ADSVKGRFTISRDNSKNTLYLQMNSLTAXDTAVYYCAKGVTGSPTLDYWGQGTLVTVSS 119
```

RESULT 4
ABR55789
ID ABR55789 standard; protein; 123 AA.
XX
AC ABR55789;
XX
DT 02-SEP-2003 (first entry)
XX
DE Heavy chain variable region of anti-Ang-2 antibody 545 HC.
XX
KW Ang-2; angiopoietin-2; anorectic; cytostatic; antiarteriosclerotic;
KW gynaecological; antiinflammatory; osteopathic; antipsoriatic; cancer;
KW angiogenesis; antibody.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Region 26. .36
FT /note= "complementarity determining region (CDR) 1"
FT Region 50. .66
FT /note= "complementarity determining region (CDR) 2"
FT Region 96. .113
FT /note= "complementarity determining region (CDR) 3"
XX
PN WO2003030833-A2.
XX
PD 17-APR-2003.
XX
PF 11-OCT-2002; 2002WO-US032613.
XX
PR 11-OCT-2001; 2001US-0328604P.
PR 10-OCT-2002; 2002US-00269805.
XX
PA (AMGE-) AMGEN INC.
XX
PI Oliner JD;
XX
DR WPI; 2003-504963/47.
XX
PT New specific binding agents (i.e. anti-Angiopoietin-2 antibodies), useful
PT for inhibiting undesired angiogenesis, or treating e.g. cancers, obesity,
PT hemangioma, arteriosclerosis, atherosclerosis or endometriosis.
XX
PS Claim 1; Page 91; 161pp; English.
XX
CC The invention relates to a specific binding agent, which comprises at
CC least one peptide selected from any of 62 peptides (ABR55769-830) or its
CC fragment. The binding agents are antibodies that recognize and bind to
CC angiopoietin-2 (Ang-2). The specific binding agent, particularly the
CC antibody, is useful for inhibiting undesired angiogenesis, treating
CC cancers, inhibiting undesired angiogenesis, modulating or inhibiting Ang-
CC 2 activity, modulating vascular permeability or plasma leakage, or
CC treating a disease (e.g. ocular neovascular disease, obesity,
CC haemangioblastoma, haemangioma, arteriosclerosis, inflammatory disease,
CC inflammatory disorders, atherosclerosis, endometriosis, neoplastic
CC disease, bone-related disease, or psoriasis) in a mammal. The present
CC sequence represents a heavy chain variable region of an anti-Ang-2
CC antibody
XX
SQ Sequence 123 AA;

Query Match 88.5%; Score 544; DB 6; Length 123;
Best Local Similarity 87.0%; Pred. No. 5e-43;
Matches 107; Conservative 1; Mismatches 11; Indels 4; Gaps 1;

```
Qy          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSSGMHWVRQAPGKGLEWVAXISYDGSRKYY 60
              |||| |||||||||||||||||||||||||| |||||||||||||||| |||||| |||
Db          1 QVQLQESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVISYDGSNKYY 60

Qy         61 ADSVKGRFTISRDNSKNTLYLQMNSLTAXDTAVYYCAKGVT----GSPTLDYWGQGTLVT 116
              |||||||||||||||||||||||| | |||||||||    |   :|||||||||
Db         61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKGPVDFDYGDYAIDYWGQGTLVT 120

Qy        117 VSS 119
              |||
Db        121 VSS 123
```

RESULT 5
AAY56287
ID AAY56287 standard; protein; 254 AA.

```
XX
AC   AAY56287;
XX
DT   08-FEB-2000  (first entry)
XX
DE   HCAT1 clone 25 antibody variable heavy chain protein sequence.
XX
KW   Human cationic amino acid transporter; hCAT1; targeted delivery;
KW   gene delivery; virus-like particle; retroviral envelope molecule;
KW   infection; gene therapy; restenosis; balloon angioplasty;
KW   smooth muscle cell; transduction.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   EP959136-A1.
XX
PD   24-NOV-1999.
XX
PF   20-MAY-1998;   98EP-00201693.
XX
PR   20-MAY-1998;   98EP-00201693.
XX
PA   (INTR-) INTROGENE BV.
XX
DR   WPI; 2000-001283/01.
DR   N-PSDB; AAZ38770.
XX
PT   New virus-like particle or gene delivery vehicle, useful for gene
PT   therapy.
XX
PS   Claim 13; Fig 16; 66pp; English.
XX
CC   The present invention describes a virus-like particle or gene delivery
CC   vehicle comprising a ligand capable of binding to a human amino acid
CC   transporter. The method is useful for the target delivery of substances
CC   to cells e.g. gene therapy. A human cationic amino acid transporter
CC   (hCAT1) targeted adenovirus is useful for local applications of
CC   adenoviral vector e.g. in patients with restenosis following balloon
CC   angioplasty where smooth muscle cells need to be transduced with an
CC   adenoviral vector carrying the CeNOS cDNA. More efficient transduction of
CC   tissues can be carried out therefore resulting in lower multiplicity's of
CC   infections that can be used and therefore less vector associated toxicity
CC   to the tissues surrounding the target cells. AAZ38737 to AAZ38770, and
CC   AAY56264 to AAY56287 represent sequences used in the exemplification of
CC   the present invention
XX
SQ   Sequence 254 AA;

  Query Match             88.2%;  Score 542.5;  DB 3;  Length 254;
  Best Local Similarity   87.5%;  Pred. No. 1.5e-42;
  Matches  105;  Conservative    5;  Mismatches    9;  Indels    1;  Gaps    1;

Qy          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSSGMHWVRQAPGKGLEWVAXISYDGSRKYY 60
              |||||:||||||||||||||||||||||  ||||||||||||||| |||||| |||
Db         23 QVQLVQSGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYY 82

Qy         61 ADSVKGRFTISRDNSKNTLYLQMNSLTAXDTAVYYCAKGVTGSPT-LDYWGQGTLVTVSS 119
              |||||||||||||||||||||||| | ||||||||:|:| : :  ||||||||||||
Db         83 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARGITVTKSRFDYWGQGTLVTVSS 142


RESULT 6
AAY56637
ID   AAY56637 standard; protein; 490 AA.
XX
AC   AAY56637;
XX
DT   22-FEB-2000  (first entry)
XX
DE   hCAT1 binding human antibody molecule protein sequence.
XX
KW   Virus-like particle; ligand; gene delivery; envelope protein; hCAT1;
KW   human cationic amino acid transporter 1; retrovirus; adenovirus;
KW   targeted delivery; gene therapy; balloon angioplasty.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   EP960942-A2.
XX
PD   01-DEC-1999.
XX
PF   20-MAY-1999;   99EP-00201593.
XX
PR   20-MAY-1998;   98EP-00201693.
XX
PA   (INTR-) INTROGENE BV.
XX
PI   Van Es H,  Verlinden S,  Havenga M;
XX
DR   WPI; 2000-025491/03.
DR   N-PSDB; AAZ38921.
XX
PT   New gene therapy vectors, useful for treating balloon angioplasty
PT   patients.
XX
PS   Claim 13; Fig 16; 50pp; English.
XX
CC   The present invention describes a virus-like particle or gene delivery
CC   vehicle (I) provided with a ligand capable of binding to a human amino
CC   acid transporter. (I) is used to deliver genes to human cells or primate
CC   cells that express the hCAT1 amino acid transporter, such as endothelial,
CC   haematopoietic or smooth muscle cells, as part of a gene therapy regime.
CC   The vectors are especially useful for providing local applications of
CC   adenoviral vector to patients with restenosis following balloon
CC   angioplasty, where smooth muscle cells need to be transduced with ceNOS
CC   cDNA, for example. (I) may also be used to pseudotype recombinant type C
CC   retrovirus including murine leukemia retroviruses and lentiviruses. In
CC   addition (I) may be used in functional genomics where transduction of as
CC   many cell types as possible is required. The new gene delivery vehicles
CC   transduce DNA more efficiently and specifically into tissues that are
CC   hard to transform, such as endothelial cells or smooth muscle cells as
CC   compared to a wildtype adenoviral vector. This increased specificity
CC   results in lower multiplicities of infection which can occur with prior
CC   art vectors, so preventing tissue toxicity. In addition the new vectors
CC   allow DNA to be transduced into cells that are in low abundance in cell
CC   mixtures and tissues, which increases their efficiency for use as gene
CC   therapy vehicles. The alteration of the ligand on the viral envelope
CC   increases the potential host cell range of these vehicles. The present
CC   sequence represents a hCAT1 binding human antibody molecule from the
CC   present invention
XX
SQ   Sequence 490 AA;

  Query Match             88.2%;  Score 542.5;  DB 3;  Length 490;
  Best Local Similarity   87.5%;  Pred. No. 3.1e-42;
  Matches  105;  Conservative    5;  Mismatches    9;  Indels    1;  Gaps    1;

Qy          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSSGMHWVRQAPGKGLEWVAXISYDGSRKYY 60
              |||||:||||||||||||||||||||||  ||||||||||||||| |||||| |||
Db        259 QVQLVQSGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYY 318

Qy         61 ADSVKGRFTISRDNSKNTLYLQMNSLTAXDTAVYYCAKGVTGSPT-LDYWGQGTLVTVSS 119
              |||||||||||||||||||||||| | ||||||||:|:| : :  ||||||||||||
Db        319 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARGITVTKSRFDYWGQGTLVTVSS 378


RESULT 7
ADA89174
ID   ADA89174 standard; protein; 120 AA.
XX
AC   ADA89174;
XX
DT   20-NOV-2003  (first entry)
XX
```

```
DE   Human antibody 1A9 heavy chain amino acid sequence SEQ ID NO:18.
XX
KW   immunoglobulin; Ig; heavy chain variable domain;
KW   light chain variable domain; major histocompatibility complex; MHC;
KW   gp100; MUC1; TAX; hTERT; cytostatic; gene therapy; cancerous disorder;
KW   cancer.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   WO2003070752-A2.
XX
PD   28-AUG-2003.
XX
PF   20-FEB-2003; 2003WO-US005128.
XX
PR   20-FEB-2002; 2002US-0358994P.
XX
PA   (DYAX-) DYAX CORP.
PA   (TECR ) TECHNION RES & DEV FOUND LTD.
XX
PI   Hoogenboom HRJM,  Reiter Y;
XX
DR   WPI; 2003-663847/62.
DR   N-PSDB; ADA89173.
XX
PT   New protein comprising an immunoglobulin heavy chain variable (VH) domain
PT   and an immunoglobulin light chain variable (VL) domain, useful for
PT   preparing a composition for treating or preventing a cancerous disorder.
XX
PS   Disclosure; Fig 3B; 224pp; English.
XX
CC   The present invention describes a protein comprising an immunoglobulin
CC   (Ig) heavy chain variable (VH) domain and an Ig light chain variable (VL)
CC   domain. The protein binds a complex comprising a major histocompatibility
CC   complex (MHC) and a peptide, does not substantially bind the MHC in the
CC   absence of the bound peptide, and does not substantially bind the peptide
CC   in the absence of the MHC. The peptide is a peptide fragment of gp100,
CC   MUC1, TAX or hTERT. ALso described: (1) a pharmaceutical composition
CC   comprising the novel protein and a carrier; (2) a cytotoxic T cell
CC   comprising one or more nucleic acids for expressing the Ig that binds a
CC   complex having an MHC and a peptide, does not substantially bind the MHC
CC   in the absence of the bound peptide, and does not substantially bind the
CC   peptide in the absence of the MHC; (3) an isolated nucleic acid
CC   comprising a first segment that encodes the Ig variable domain; (4) a
CC   host cell comprising heterologous nucleic acid sequences that encodes the
CC   novel protein; (5) a transgenic animal whose genome includes heterologous
CC   nucleic acid sequences that encode the protein; (6) identifying the
CC   protein that specifically binds the MHC-peptide complex; (7) expressing
CC   an antigen-binding protein; (8) ablating or killing a target cell that
CC   displays a peptide on a surface MHC molecule; (9) treating or preventing
CC   a cancerous disorder in a subject; and (10) detecting an MHC-peptide
CC   complex in a sample. A protein of the invention has cytostatic activity,
CC   and can be used in gene therapy. The protein is useful for preparing a
CC   composition for treating or preventing a cancerous disorder. The present
CC   sequence represents the heavy chain of an antibody which binds to an MHC-
CC   peptide complex where the peptide component in as peptide fragment of
CC   gp100.
XX
SQ   Sequence 120 AA;

  Query Match             87.9%;  Score 540.5;  DB 6;  Length 120;
  Best Local Similarity   88.3%;  Pred. No. 1e-42;
  Matches  106;  Conservative    2;  Mismatches   11;  Indels    1;  Gaps    1;

Qy          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSSGMHWVRQAPGKGLEWVAXISYDGSRKYY 60
              |||||:|||||||||||||||||||||||| |||||||||||||||| |||||| |||
Db          1 QVQLVQSGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVISYDGSNKYY 60

Qy         61 ADSVKGRFTISRDNSKNTLYLQMNSLTAXDTAVYYCAKGVTGS-PTLDYWGQGTLVTVSS 119
              |||||||||||||||||||||||| | ||||||||:   |    ||||||||||||||
Db         61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDYYGDYALLDYWGQGTLVTVSS 120
```

```
RESULT 8
ADP47108
ID   ADP47108 standard; protein; 121 AA.
XX
AC   ADP47108;
XX
DT   09-SEP-2004  (first entry)
XX
DE   Human phospholipase A2-specific monoclonal antibody heavy chain #11.
XX
KW   human; monoclonal antibody; phospholipase A2; PLA2;
KW   inflammatory disorder; degenerative disorder;
KW   joint inflammatory reaction; skin inflammatory reaction;
KW   blood vessels inflammatory reaction; arthritis; psoriasis; asthma;
KW   Alzheimer's disease; atherosclerosis; restenosis; heavy chain.
XX
OS   Homo sapiens.
XX
PN   WO2004050850-A2.
XX
PD   17-JUN-2004.
XX
PF   02-DEC-2003; 2003WO-US038234.
XX
PR   02-DEC-2002; 2002US-0430724P.
XX
PA   (ABGE-) ABGENIX INC.
PA   (LEXI-) LEXICON GENETICS INC.
XX
PI   Landes GM,  Haak-Frendscho M,  Chen L,  Lee YR,  Liang ML,  Feng X;
PI   Jia X,  Nocerini MR;
XX
DR   WPI; 2004-461119/43.
XX
PT   New human monoclonal antibody that binds to phospholipase A2 (PLA2),
PT   useful for treating inflammatory conditions, e.g. arthritis, psoriasis,
PT   asthma, Alzheimer's disease, atherosclerosis, or restenosis.
XX
PS   Claim 1; SEQ ID NO 23; 128pp; English.
XX
CC   The invention comprises a human monoclonal antibody that binds to
CC   phospholipase A2 (PLA2). The monoclonal antibody of the invention is
CC   useful in the preparation of a medicament for the treatment of
CC   inflammatory and degenerative disorders stemming from inflammatory
CC   reactions in the joints, skin, and blood vessels, arthritis, psoriasis,
CC   asthma, Alzheimer's disease, atherosclerosis, and restenosis. The present
CC   amino acid sequence represents the heavy chain from a monoclonal antibody
CC   that is specific for the human phospholipase A2 (PLA2) enzyme.
XX
SQ   Sequence 121 AA;

  Query Match             87.9%;  Score 540.5;  DB 8;  Length 121;
  Best Local Similarity   87.5%;  Pred. No. 1e-42;
  Matches  105;  Conservative    4;  Mismatches   10;  Indels    1;  Gaps    1;

Qy          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSSGMHWVRQAPGKGLEWVAXISYDGSRKYY 60
              |||||||||||||||||||||||||||||||| |||||||||||||||| | |||| |:|
Db          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAAIWYDGSNKWY 60

Qy         61 ADSVKGRFTISRDNSKNTLYLQMNSLTAXDTAVYYCAKGVTGSP-TLDYWGQGTLVTVSS 119
              |||||||||||||||||||||||| | ||||||||:| ||:|    | |||||:|||||
Db         61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARGGTGTPGAFDIWGQGTMVTVSS 120
```

```
RESULT 9
ADP22284
ID   ADP22284 standard; protein; 121 AA.
XX
AC   ADP22284;
XX
DT   09-SEP-2004  (first entry)
XX
```

DE Human anti-TNFa antibody heavy chain variable region SEQ ID NO:190.
XX
KW human; monoclonal antibody; tumour necrosis factor-alpha; TNFa;
KW anti-TNFa antibody; anabolic; antiarteriosclerotic; antiarthritic;
KW antibacterial; antiinflammatory; antipsoriatic; antirheumatic;
KW eating-disorder; immunomodulator; immunosuppressive; nephrotropic;
KW neuroprotective; vasotropic; antiapoptotic; TNFa antagonist;
KW TNF induced apoptosis; neoplastic disease; breast cancer; ovarian cancer;
KW bladder cancer; lung cancer; glioblastoma; stomach cancer;
KW endometrial cancer; kidney cancer; colon cancer; pancreatic cancer;
KW prostrate cancer; immuno-mediated inflammatory disease;
KW rheumatoid arthritis; glomerulonephritis; atherosclerosis; psoriasis;
KW restenosis; autoimmune disease; Crohn's disease; graft-host reaction;
KW septic shock; cachexia; anorexia; multiple sclerosis.
XX
OS Homo sapiens.
XX
PN WO2004050683-A2.
XX
PD 17-JUN-2004.
XX
PF 02-DEC-2003; 2003WO-US038281.
XX
PR 02-DEC-2002; 2002US-0430729P.
XX
PA (ABGE-) ABGENIX INC.
XX
PI Babcook JS, Kang JS, Foord O, Green L, Feng X, Klakamp S;
PI Haak-Frendscho M, Rathanaswami P, Pigott C, Liang ML, Lee R;
PI Manchulencho K, Faggioni R, Senaldi G, Qiaojuan JS;
XX
DR WPI; 2004-480601/45.
DR N-PSDB; ADP22283.
XX
PT New recombinant human monoclonal antibody that specifically binds to
PT Tumor Necrosis Factor-alpha, useful for treating neoplastic disease such
PT as cancers, or immuno-mediated inflammatory diseases such as rheumatoid
PT arthritis.
XX
PS Example 10; SEQ ID NO 190; 213pp; English.
XX
CC The present invention describes a human monoclonal antibody (I) that
CC specifically binds to tumour necrosis factor-alpha (TNFa) and comprises:
CC (a) a heavy chain complementarity determining region 1 (CDR1) having the
CC two fully defined 5 amino acid sequence (S1, ADP22417) or (S2, ADP22421);
CC and (b) a light chain CDR1 having the two fully defined 11 amino acid
CC sequence (S3, ADP22418) or (S4, ADP22424). Also described: (1) assaying
CC (M1) the level of TNFa in a patient sample, comprising contacting with
CC (I), and detecting the level of binding between the antibody and TNFa in
CC the sample; (2) a composition comprising the antibody or its functional
CC fragment and a carrier; (3) treating (M2) an animal suffering from a
CC neoplastic, or an immuno-mediated inflammatory disease by selecting an
CC animal in need of treatment for the disease by administering the human
CC monoclonal antibody of (I); and (4) inhibiting (M3) TNFa induced
CC apoptosis in an animal by selecting an animal in need of treatment for
CC TNFa induced apoptosis by administering the human monoclonal antibody of
CC (I). (I) has anabolic, antiarteriosclerotic, antiarthritic,
CC antibacterial, antiinflammatory, antipsoriatic, antirheumatic, eating-
CC disorders, immunomodulator, immunosuppressive, nephrotropic,
CC neuroprotective, vasotropic and antiapoptotic activities, and can be used
CC as a TNFa antagonist. The antibody (I) is useful in the preparation of
CC medicament for treating TNF induced apoptosis, neoplastic disease such as
CC breast cancer, ovarian cancer, bladder cancer, lung cancer, glioblastoma,
CC stomach cancer, endometrial cancer, kidney cancer, colon cancer,
CC pancreatic cancer, and prostrate cancer; or immuno-mediated inflammatory
CC diseases such as rheumatoid arthritis, glomerulonephritis,
CC atherosclerosis, psoriasis, restenosis, autoimmune disease, Crohn's
CC disease, graft-host reactions, septic shock, cachexia, anorexia, and
CC multiple sclerosis. The present sequence represents a human anti-TNFa
CC antibody heavy chain variable region, which is used in the
CC exemplification of the present invention.
XX
SQ Sequence 121 AA;

```
  Query Match             87.8%;  Score 540;  DB 8;  Length 121;
  Best Local Similarity   87.6%;  Pred. No. 1.2e-42;
  Matches  106;  Conservative    2;  Mismatches   11;  Indels    2;  Gaps    1;

Qy          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSSGMHWVRQAPGKGLEWVAXISYDGSRKYY 60
              |||||||||||||||||||||||||||||| |||||||||||||||| | |||| |||
Db          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVIWYDGSNKYY 60

Qy         61 ADSVKGRFTISRDNSKNTLYLQMNSLTAXDTAVYYCAK--GVTGSPTLDYWGQGTLVTVS 118
              |||||||||||||||||||||||| | |||||||:     |:|  ||||||||||||
Db         61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAREGDYGGNPYFDYWGQGTLVTVS 120

Qy        119 S 119
              |
Db        121 S 121
```

RESULT 10
AAE32095
ID AAE32095 standard; protein; 119 AA.
XX
AC AAE32095;
XX
DT 24-MAR-2003 (first entry)
XX
DE Human VEGF-2 hybridoma antibody #1.
XX
KW Human; vascular endothelial growth factor; VEGF-2; inflammatory disease;
KW proliferative disorder; tumour; breast; cancer; brain; prostate; colon;
KW lymphangioma; infection; Kaposi's sarcoma; psoriasis; immunosuppressive;
KW rheumatoid arthritis; diabetic retinopathy; gene therapy; antimicrobial;
KW cytostatic; ophthalmological; antibody; autoimmune disease.
XX
OS Homo sapiens.
XX
PN WO200283849-A2.
XX
PD 24-OCT-2002.
XX
PF 12-APR-2002; 2002WO-US011404.
XX
PR 13-APR-2001; 2001US-0283391P.
PR 07-SEP-2001; 2001US-0317600P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Albert VR, Ruben SM, Wager RE;
XX
DR WPI; 2003-093007/08.
DR N-PSDB; AAD49586.
XX
PT New vascular endothelial growth factor (VEGF)- 2 antibodies, for
PT treating, preventing or ameliorating a disease or disorder, such as
PT inflammatory diseases, proliferative disorders, autoimmune disorders or
PT diabetic retinopathy.
XX
PS Disclosure; Page 394; 399pp; English.
XX
CC The invention relates to vascular endothelial growth factor (VEGF)-2
CC antibodies. VEGF-2 antibodies are useful for treating, preventing or
CC ameliorating a disease or disorder, such as inflammatory diseases or
CC disorders, proliferative disorders, tumours, tumour metastasis, breast
CC cancer, brain cancer, prostate cancer, colon cancer, lymphangioma, an
CC infectious disease, Kaposi's sarcoma, an autoimmune disease, rheumatoid
CC arthritis, psoriasis, diabetic retinopathy, a disease or disorder
CC associated with aberrant VEGF-2 (receptor) expression, or a disease or
CC disorder associated with the lack of VEGF-2 (receptor) function. The
CC antibody is also useful for detecting, diagnosing, prognosing, or
CC monitoring cancers and other hyperproliferative disorders. VEGF-2 is also
CC used in gene therapy. The present sequence is human VEGF-2 hybridoma
CC antibody
XX

```
SQ   Sequence 119 AA;

  Query Match             87.6%;  Score 539;  DB 6;  Length 119;
  Best Local Similarity   88.2%;  Pred. No. 1.4e-42;
  Matches  105;  Conservative    1;  Mismatches   13;  Indels    0;  Gaps    0;

Qy          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSSGMHWVRQAPGKGLEWVAXISYDGSRKYY 60
              |||||||||||||||||||||||||||||  |||||||||||||||| | |||| |||
Db          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSRYGMHWVRQAPGKGLEWVALIWYDGSNKYY 60

Qy         61 ADSVKGRFTISRDNSKNTLYLQMNSLTAXDTAVYYCAKGVTGSPTLDYWGQGTLVTVSS 119
              |||||||||||||||||||||||||| | ||||||||:   ||   ||||||||||||
Db         61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDGFGSGCFDYWGQGTLVTVSS 119


RESULT 11
ABG30463
ID   ABG30463 standard; protein; 118 AA.
XX
AC   ABG30463;
XX
DT   07-OCT-2002  (first entry)
XX
DE   Human anti-CD40 monoclonal antibody 9F7 VH.1 region.
XX
KW   Human; VH.1; heavy chain variable region; CD40; autoimmune disease;
KW   systemic lupus erythematosus; psoriasis; multiple sclerosis;
KW   inflammatory bowel disease; Crohn's disease; rheumatoid arthritis;
KW   organ rejection; lymphoma; non-Hodgkin's lymphoma; monoclonal antibody;
KW   B cell; glycoprotein; proliferation.
XX
OS   Homo sapiens.
XX
PN   WO200228904-A2.
XX
PD   11-APR-2002.
XX
PF   02-OCT-2001; 2001WO-US030857.
XX
PR   02-OCT-2000; 2000US-0237556P.
XX
PA   (CHIR ) CHIRON CORP.
XX
PI   Chu K,  Wang C,  Yoshihara C,  Donnelly JJ;
XX
DR   WPI; 2002-405169/43.
DR   N-PSDB; ABK88453.
XX
PT   A human anti-CD40 monoclonal antibody or fragment useful for inhibiting
PT   proliferation, growth or differentiation of a normal human B cells and
PT   treating autoimmune disease such as rheumatoid arthritis or systemic
PT   lupus erythematosus.
XX
PS   Claim 6; Fig 14; 75pp; English.
XX
CC   The invention relates to a human monoclonal antibody or fragment capable
CC   of specifically binding to a human CD40 antigen (a glycoprotein expressed
CC   on the surface of human B cells), where the antibody or fragment is free
CC   of significant agonistic activity when it binds to the CD40 antigen, and
CC   the growth or differentiation is inhibited. The fragments comprise the
CC   complementarity determining region (CDR) of the light and heavy chains of
CC   the monoclonal antibodies secreted by a hybridoma consisting of 15B8,
CC   20C4, 12D9, 9F7 and 13E4. Also included are the nucleic acids encoding
CC   the antibody (or fragments). The antibodies or fragments are used for
CC   inhibiting proliferation, growth or differentiation of a normal human B
CC   cells and to inhibit antibody production by B cells. They may also be
CC   useful for treating autoimmune diseases, such as systemic lupus
CC   erythematosus, psoriasis, multiple sclerosis, inflammatory bowel disease
CC   (Crohn's disease), rheumatoid arthritis, and lymphoma (especially Non-
CC   Hodgkin's Lymphoma). The present sequence represents the antibody 9F7
CC   heavy chain variable region VH.1
XX
SQ   Sequence 118 AA;

  Query Match             87.6%;  Score 538.5;  DB 5;  Length 118;
  Best Local Similarity   89.9%;  Pred. No. 1.6e-42;
  Matches  107;  Conservative    1;  Mismatches   10;  Indels    1;  Gaps    1;

Qy          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSSGMHWVRQAPGKGLEWVAXISYDGSRKYY 60
              |||| |||||||||||||||||||||||| |||||||||||||||| |||||| |||
Db          1 QVQLQESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVISYDGSIKYY 60

Qy         61 ADSVKGRFTISRDNSKNTLYLQMNSLTAXDTAVYYCAKGVTGSPTLDYWGQGTLVTVSS 119
              |||||||||||||||||||||||||| | ||||||||:   ||   ||||||||||||
Db         61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARD-HGSNPLDYWGQGTLVTVSS 118


RESULT 12
ADG30467
ID   ADG30467 standard; protein; 241 AA.
XX
AC   ADG30467;
XX
DT   26-FEB-2004  (first entry)
XX
DE   Human GMBC683 scFv protein.
XX
KW   GMAD; VH; CDR; complementarity determining region; VL; scFv;
KW   single chain antibody; antidiabetic; type II diabetes; human; GMBC683.
XX
OS   Homo sapiens.
XX
PN   WO2003085093-A2.
XX
PD   16-OCT-2003.
XX
PF   28-MAR-2003; 2003WO-US009625.
XX
PR   01-APR-2002; 2002US-0368813P.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
XX
PI   Baker KP,  Albert VR,  Chowdhury P;
XX
DR   WPI; 2003-804305/75.
DR   N-PSDB; ADG30564.
XX
PT   New antibody that specifically binds to GMAD polypeptide, useful for
PT   diagnosing, monitoring, treating, preventing or ameliorating type II
PT   diabetes.
XX
PS   Claim 2; SEQ ID NO 100; 410pp; English.
XX
CC   The invention relates to a novel antibody that specifically binds to a
CC   GMAD polypeptide comprising a first amino acid sequence that is at least
CC   95% identical to a second amino acid sequence of a VH CDR
CC   (complementarity determining region) or VL CDR of an scFv (single chain
CC   antibody molecule). The antibody of the invention demonstrates
CC   antidiabetic activity and may be useful for diagnosing, monitoring,
CC   treating, preventing or ameliorating type II diabetes. The current
CC   sequence is that of the human scFv protein of the invention.
XX
SQ   Sequence 241 AA;

  Query Match             87.6%;  Score 538.5;  DB 7;  Length 241;
  Best Local Similarity   88.2%;  Pred. No. 3.4e-42;
  Matches  105;  Conservative    2;  Mismatches   11;  Indels    1;  Gaps    1;

Qy          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSSGMHWVRQAPGKGLEWVAXISYDGSRKYY 60
              :|||||||||:|||||||||||||||||||| |||||||||||||||| |||||| |||
Db          1 EVQLVESGGGLVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVISYDGSNKYY 60

Qy         61 ADSVKGRFTISRDNSKNTLYLQMNSLTAXDTAVYYCAKGVTGSPTLDYWGQGTLVTVSS 119
              |||||||||||||||||||||||||| | |||||||||      |||||||| |||||
Db         61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKRAAAG-TLDYWGQGTTVTVSS 118
```

RESULT 13
ADO36354
ID ADO36354 standard; protein; 117 AA.
XX
AC ADO36354;
XX
DT 26-AUG-2004 (first entry)
XX
DE Intracellular interaction-related scFv protein SeqID18.
XX
KW immunoglobulin single domain; intracellular environment;
KW intracellular interaction; immunoglobulin domain; scFv;
KW single chain variable fragment.
XX
OS Unidentified.
XX
PN WO2004046185-A2.
XX
PD 03-JUN-2004.
XX
PF 14-NOV-2003; 2003WO-GB004942.
XX
PR 15-NOV-2002; 2002GB-00026729.
XX
PA (MEDI-) MEDICAL RES COUNCIL.
XX
PI Rabbitts TH, Tanaka T;
XX
DR WPI; 2004-431946/40.
XX
PT Determining the ability of an immunoglobulin single domain to bind to a
PT target in an intracellular environment by assessing the intracellular
PT interaction between the immunoglobulin domain and the target by
PT monitoring the signal.
XX
PS Disclosure; SEQ ID NO 18; 66pp; English.
XX
CC This invention relates to a novel method of determining the ability of an
CC immunoglobulin single domain to bind to a target in an intracellular
CC environment comprising assessing the intracellular interaction between
CC the immunoglobulin domain and the target by monitoring the signal. The
CC method comprises providing a first molecule and a second molecule, where
CC stable interaction of the first and second molecules leads to the
CC generation of a signal; providing a single intracellular immunoglobulin
CC domain which is associated with the first molecule, where the single
CC immunoglobulin domain is free of complementary immunoglobulin domains;
CC providing an intracellular target which is associated with the second
CC molecule, such that association of the immunoglobulin domain and the
CC target leads to stable interaction of the first and second molecules and
CC generation of the signal; and assessing the intracellular interaction
CC between the immunoglobulin domain and the target by monitoring the
CC signal. The methods are useful for determining the ability of an
CC immunoglobulin single domain to bind to a target in an intracellular
CC environment. The present sequence is that of a single chain variable
CC fragment (scFv) protein which was used to illustrate the method of the
CC invention.
XX
SQ Sequence 117 AA;

Query Match 87.5%; Score 538; DB 8; Length 117;
Best Local Similarity 89.2%; Pred. No. 1.7e-42;
Matches 107; Conservative 1; Mismatches 8; Indels 4; Gaps 2;

```
Qy          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSSGMHWVRQAPGKGLEWVAXISYDGSRKYY 60
              |||||||||||||||||||||||||||||| ||||||||||||||: |||||| |||
Db          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVSVISYDGSNKYY 60

Qy         61 ADSVKGRFTISRDNSKNTLYLQMNSLTAXDTAVYYCAKGVTGSPT-LDYWGQGTLVTVSS 119
              ||||||||||||||||||||||||| | |||||||||    ||   |||||||||||||
Db         61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAK---ASPLHFDYWGQGTLVTVSS 117
```

RESULT 14
ADL91327
ID ADL91327 standard; protein; 119 AA.
XX
AC ADL91327;
XX
DT 20-MAY-2004 (first entry)
XX
DE VH chain clone A20 of an intracellularly binding immunoglobulin SeqID 18.
XX
KW antibody; variable chain; cytostatic; cytoplasmic degradation;
KW intracellular relocation; specific antigen positive cancer; leukaemia;
KW lymphoma; intracellularly binding immunoglobulin; BCR-ABL.
XX
OS Unidentified.
XX
PN WO2003077945-A1.
XX
PD 25-SEP-2003.
XX
PF 14-MAR-2003; 2003WO-GB001077.
XX
PR 14-MAR-2002; 2002GB-00006043.
PR 15-NOV-2002; 2002GB-00026723.
PR 15-NOV-2002; 2002GB-00026727.
XX
PA (MEDI-) MEDICAL RES COUNCIL.
XX
PI Lobato-Caballero MN, Rabbitts TH;
XX
DR WPI; 2003-779088/73.
XX
PT Use of an intracellularly binding immunoglobulin comprising at least one
PT antibody variable chain, in preparing a medicament for degrading one or
PT more specific antigens, or for treating specific antigen positive cancer,
PT e.g. leukemia.
XX
PS Example 1; SEQ ID NO 18; 86pp; English.
XX
CC This invention relates to novel immunoglobulin molecules that comprise at
CC least one antibody variable chain VH or VL framework region and are
CC capable of binding to a specific antigens within an intracellular
CC environment. Specifically, it refers to antibodies that can form an
CC insoluble complex with a cognate antigen, such that it can then be target
CC for degradation via the lysosome or proteosome systems. The present
CC invention describes the specific target antigen as the oncogenic fusion
CC protein BCR-ABL or the RAS antigen, such that this method can be used to
CC prepare a cytostatic medicament for the cytoplasmic degradation or
CC intracellular relocation of such an antigen or for the treatment of the
CC specific antigen positive cancer i.e. leukaemia or lymphoma. Furthermore,
CC the immunoglobulins may also be used for therapeutic, prophylactic or
CC diagnostic applications both in vitro and in vivo, as well as for assay
CC and reagent applications or in functional genomics. This polypeptide
CC sequence is a variable heavy chain (VH) framework region of an
CC intracellularly binding anti-ABL antibody of the invention.
XX
SQ Sequence 119 AA;

Query Match 87.5%; Score 538; DB 7; Length 119;
Best Local Similarity 89.2%; Pred. No. 1.8e-42;
Matches 107; Conservative 1; Mismatches 8; Indels 4; Gaps 2;

```
Qy          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSSGMHWVRQAPGKGLEWVAXISYDGSRKYY 60
              |||||||||||||||||||||||||||||| ||||||||||||||: |||||| |||
Db          3 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVSVISYDGSNKYY 62

Qy         61 ADSVKGRFTISRDNSKNTLYLQMNSLTAXDTAVYYCAKGVTGSPT-LDYWGQGTLVTVSS 119
              ||||||||||||||||||||||||| | |||||||||    ||   |||||||||||||
Db         63 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAK---ASPLHFDYWGQGTLVTVSS 119
```

RESULT 15
ABM82698

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ID   ABM82698 standard; protein; 583 AA.
XX
AC   ABM82698;
XX
DT   18-NOV-2004  (first entry)
XX
DE   Human diagnostic and therapeutic pprotein SEQ ID NO:2947.
XX
KW   gene therapy; human diagnostic and therapeutic polynucleotide; dithp.
XX
OS   Homo sapiens.
XX
PN   WO2004023973-A2.
XX
PD   25-MAR-2004.
XX
PF   12-SEP-2003; 2003WO-US028227.
XX
PR   12-SEP-2002; 2002US-0410259P.
PR   12-SEP-2002; 2002US-0410260P.
XX
PA   (INCY-) INCYTE CORP.
XX
PI   Schmidt JP,  Wright RJ,  Bruns CM,  Marjanovic MM,  Shen F;
PI   Harthshorne TA,  Suchorolski MT,  Altus CM,  Pitts SJ,  Elder LV;
PI   Mooney EM,  Delegeane AM,  Panesar IS,  Banville SC,  Reddy TP;
PI   Stevens KA,  Blanchard JL,  Panzer SR,  Wang X,  Au AP,  Gerstin EH;
PI   Peralta CH,  Anderson SB,  Rioux P,  Shen EJ,  Wu MC,  Stuve LL;
PI   Lagace RE,  Spiro PA,  Stewart EA,  Wingrove J,  Vitt UA,  Kirton ES;
PI   Xu Y,  Kwong M,  Policky JL,  Hurwitz BL,  Ma Y,  Jackson JL,  Gietzen D;
PI   Patury S,  Shi X,  Suarez CJ;
XX
DR   WPI; 2004-329368/30.
DR   N-PSDB; ACN41350.
XX
PT   New diagnostic and therapeutic polynucleotides and polypeptides, useful
PT   in diagnosing a condition, disease or disorder associated with human
PT   molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or
PT   in gene mapping.
XX
PS   Claim 27; Page; 190pp; English.
XX
CC   The invention relates to novel diagnostic and therapeutic polynucleotides
CC   selected from one of the 2722 sequences defined in the specification. A
CC   polynucleotide of the invention may have a use in gene therapy. The human
CC   diagnostic and therapeutic polynucleotides (dithp) or polypeptides may be
CC   used to diagnose a particular condition, disease or disorder associated
CC   with human molecules, e.g. cell proliferative disorders,
CC   autoimmune/inflammatory disorder, developmental disorder, endocrine
CC   disorder, neurological disorders, gastrointestinal disorders, or
CC   infections caused by virus, bacteria, fungi or parasite. The dithp
CC   molecules may also be used in genetic mapping, in identifying individuals
CC   from minute biological samples, in detecting single nucleotide
CC   polymorphisms, as molecular weight markers, and for somatic or germline
CC   gene therapy. The present sequence represents a dithp protein of the
CC   invention. Note: The sequence data for this patent is not represented in
CC   the printed specification, but was obtained in electronic format directly
CC   from WIPO at www.wipo.int/pct/en/sequences/listing.htm
XX
SQ   Sequence 583 AA;

  Query Match             87.4%;  Score 537.5;  DB 8;  Length 583;
  Best Local Similarity   87.7%;  Pred. No. 1.1e-41;
  Matches  107;  Conservative    1;  Mismatches    9;  Indels    5;  Gaps    2;

Qy          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSSGMHWVRQAPGKGLEWVAXISYDGSRKYY 60
              |||||||||||||||||||||||||||||| |||||||||||||||| |||||| |||
Db         20 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVISYDGSNKYY 79

Qy         61 ADSVKGRFTISRDNSKNTLYLQMNSLTAXDTAVYYCAKGVTGSPT---LDYWGQGTLVTV 117
              |||||||||||||||||||||||| | ||||||||:     ||    ||||||||||
Db         80 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDT--PPTCDYFDYWGQGTLVTV 137

Qy        118 SS 119
              ||
Db        138 SS 139


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